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OM protein - protein search, using sw model

Run on: July 27, 2005, 12:32:19 ; Search time 3.12889 Seconds
(without alignments)
381.728 Million cell updates/sec

Title: US-10-030-937-68
Perfect score: 94
Sequence: 1 FSWDCFEKDPVIR 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents:AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
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5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	90.4	178	4	US-09-183-841-2
2	85	90.4	193	4	US-09-183-841-1
3	44	46.8	406	4	US-09-599-360B-98
4	44	46.8	1765	4	US-09-270-767-45587
5	43	45.7	15	4	US-09-069-827A-129
6	43	45.7	590	2	US-08-756-317-12
7	43	45.7	619	4	US-09-489-039A-12704
8	42	44.7	119	4	US-09-270-767-47348
9	41	43.6	13	4	US-10-158-847-113
10	41	43.6	506	2	US-08-635-066-2
11	41	43.6	864	4	US-10-101-464A-896
12	41	43.6	956	4	US-09-252-991A-17124
13	40.5	43.1	246	4	US-09-602-777A-206
14	40.5	43.1	422	4	US-09-602-777A-202
15	40	42.6	19	1	US-08-469-615-18
16	40	42.6	19	2	US-08-466-763-18
17	40	42.6	19	2	US-08-411-142A-18
18	40	42.6	40	1	US-07-901-874B-5
19	40	42.6	40	1	US-08-457-865-5
20	40	42.6	304	4	US-09-710-279-2190
21	40	42.6	376	4	US-09-270-767-33947
22	40	42.6	376	4	US-09-270-767-49164
23	40	42.6	385	2	US-08-516-801-2
24	40	42.6	385	3	US-08-248-355-2
25	40	42.6	385	4	US-09-167-206-16
26	40	42.6	385	5	PCT-US95-06683-2
27	40	42.6	399	4	US-09-949-016-10810

28	40	42.6	415	3	US-09-134-001C-5077	Sequence 5077, Ap
29	40	42.6	488	1	US-07-672-483-1	Sequence 1, Appli
30	40	42.6	490	2	US-08-687-916-24	Sequence 24, Appl
31	40	42.6	490	3	US-09-138-614-24	Sequence 24, Appl
32	40	42.6	619	4	US-09-543-681A-5503	Sequence 5503, Ap
33	40	42.6	621	2	US-08-969-714-1	Sequence 1, Appli
34	40	42.6	645	2	US-08-969-714-3	Sequence 3, Appli
35	39	41.5	13	4	US-10-158-847-105	Sequence 105, App
36	39	41.5	191	4	US-09-489-039A-12833	Sequence 12833, A
37	39	41.5	242	4	US-09-270-767-32046	Sequence 32046, A
38	39	41.5	364	3	US-09-338-671-2	Sequence 2, Appli
39	39	41.5	444	1	US-08-483-140-28	Sequence 28, Appl
40	39	41.5	444	2	US-08-485-938A-32	Sequence 32, Appl
41	39	41.5	658	4	US-09-328-599A-2	Sequence 2, Appli
42	39	41.5	795	3	US-09-031-563-23	Sequence 23, Appl
43	39	41.5	795	4	US-09-392-277-23	Sequence 23, Appl
44	39	41.5	795	4	US-09-258-000-23	Sequence 23, Appl
45	39	41.5	878	4	US-09-556-706B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match 90.4%; Score 85; DB 4; Length 178;
Best Local Similarity 93.8%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FSWDCFEKDPVIR 16
||||| |||||||
DB 19 FSWDCDEGKDPVIR 34

RESULT 2
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

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; LOCATION: (33)..(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1

Query Match          90.4%; Score 85; DB 4; Length 193;
Best Local Similarity 93.8%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 FSWDNCFCGKDPAVIR 16
      ||||| ||||| |||||
Db      34 FSWDNCDEGKDPAVIR 49

RESULT 3
US-09-599-360B-98
; Sequence 98, Application US/09599360B
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
; CURRENT APPLICATION NUMBER: US/09/599,360B
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 98
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -35..-1
US-09-599-360B-98

Query Match          46.8%; Score 44; DB 4; Length 406;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 FSWDNCFCGKDPAVI 15
      ||||| : ||||
Db      155 FSWNITDSLDPATL 169

RESULT 4
US-09-270-767-45587
; Sequence 45587, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45587
; LENGTH: 1765
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45587

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; Patent No. 5849894
; GENERAL INFORMATION:
; APPLICANT: Clemente, Thomas E.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Mitsky, Timothy A.
; APPLICANT: Stark, David M.
; TITLE OF INVENTION: Improved Rhodospirillum Rubrum
; TITLE OF INVENTION: Poly-B-Hydroxyalkanoate Synthase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,317
; FILING DATE: 25-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,693
; FILING DATE: 29-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L.
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; TELEFAX: (713) 787-1440
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 590 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-756-317-12

Query Match 45.7%; Score 43; DB 2; Length 590;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 WDNCFEGKD 11
Db 486 WDTCFRGAD 494

RESULT 7
US-09-489-039A-12704
; Sequence 12704, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12704
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12704

Query Match 45.7%; Score 43; DB 4; Length 619;

Best Local Similarity 50.0%; Pred. No. 79;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 WDNCFEGKDPVIR 16
Db 478 WNNTRSGEDPVAIR 491

RESULT 8
US-09-270-767-47348
; Sequence 47348, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47348
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47348

Query Match 44.7%; Score 42; DB 4; Length 119;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 WDNCFEGKDPV 14
Db 97 WRECPEGFQFTI 108

RESULT 9
US-10-158-847-113
; Sequence 113, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-158-847-113

Query Match 43.6%; Score 41; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.7;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 FSWDNCFEG 9
Db 5 FDWDECFLG 13

RESULT 10
US-08-635-066-2
; Sequence 2, Application US/08635066
; Patent No. 5945580
; GENERAL INFORMATION:
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Hardster, Mark H.
; TITLE OF INVENTION: Capsicum Hemocellulase Polynucleotides
; TITLE OF INVENTION: and Polypeptides

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,066
FILING DATE: 19-APR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 012176-005500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 506 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-635-066-2

Query Match 43.6%; Score 41; DB 2; Length 506;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PSWDNCFEG 9
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DB 266 PSWDNKFAG 274

RESULT 11
US-10-101-464A-896
Sequence 896, Application US/10101464A
Patent No. 6768041
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101.464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PC7/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 896
LENGTH: 864
TYPE: PRT
ORGANISM: Pinus radiata
US-10-101-464A-896
Query Match 43.6%; Score 41; DB 4; Length 864;
Best Local Similarity 58.3%; Pred. NO. 2.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 NCFEGKDPVIR 16
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DB 402 NCFSGAIPSLIR 413

RESULT 12
US-09-252-991A-17124
Sequence 17124, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17124
LENGTH: 956
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17124

Query Match 43.6%; Score 41; DB 4; Length 956;
Best Local Similarity 66.7%; Pred. NO. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DNCFEGKDP 12
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DB 291 EHCFEHDP 299

RESULT 13
US-09-602-777A-206
Sequence 206, Application US/09602777A
Patent No. 6831165
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauser, Gregor
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
FILE REFERENCE: BGI-128CP
CURRENT APPLICATION NUMBER: US/09/602,777A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: DE 19932226.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932920.6
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932922.2
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932924.9


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; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 206
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-206

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Query Match 43.1%; Score 40.5; DB 4; Length 246;
Best Local Similarity 34.6%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 5; Indels 11; Gaps 1;

QY 1 FSWDNCF-----EGKDPVAVI 15
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Db 151 FSWKNCLSESGSHLPVHDGSDAVVI 176

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RESULT 14
US-09-602-777A-202
; Sequence 202, Application US/09602777A
; Patent No. 6831165
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habernauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CP
; CURRENT APPLICATION NUMBER: US/09/602,777A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9

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; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932924.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 202
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-202

Query Match 43.1%; Score 40.5; DB 4; Length 422;
Best Local Similarity 34.6%; Pred. No. 1.3e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 11; Gaps 1;

QY 1 FSWDNCF-----EGKDPVAVI 15
    ||| |||
Db 145 FSWKNCLSESGSHLPVHDGSDAVVI 170

RESULT 15
US-08-469-615-18
; Sequence 18, Application US/08469615
; Patent No. 5622703
; GENERAL INFORMATION:
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Kurata, Akihiko
; TITLE OF INVENTION: Immunodominant Sites of HTLV-I Envelope
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolaesch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/469,615
, FILING DATE: 06-JUN-1995
, CLASSIFICATION: 435
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/243,118
, FILING DATE: 16-MAY-1994
, ATTORNEY/AGENT INFORMATION:
, NAME: Svensson, Leonard R.
, REGISTRATION NUMBER: 30330
, REFERENCE/DOCKET NUMBER: 1173-500P
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 703-205-8000
, TELEFAX: 703-205-8050
, INFORMATION FOR SEQ ID NO: 18:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 19 amino acids
, TYPE: amino acid
, STRANDEDNESS: not relevant
, TOPOLOGY: not relevant
, MOLECULE TYPE: peptide
, HYPOTHETICAL: NO
, FRAGMENT TYPE: internal
, ORIGINAL SOURCE:
, ORGANISM: htlv-I
, FEATURE:
, NAME/KEY: Peptide
, LOCATION: 1..19
, OTHER INFORMATION: /label= pepcid_v1es
, US-08-469-615-18

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Query Match 42.6%; Score 40; DB 1; Length 19;
Best Local Similarity 33.3%; Pred. No. 6;
Matches 5; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy	1	FSWDNCFEGKDP	AVI	15
		: : :	:	:
Dd	4	FNWTHCFDPQIQ	AI	18

Search completed: July 27, 2005, 18:59:20
Job time : 5.12889 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:09:01 ; Search time 35.0578 Seconds
(without alignments)
177.532 Million cell updates/sec

Title: US-10-030-937-68

Perfect score: 94

Sequence: 1 FSWNCFEGKPAVIR 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	90.4	193	15	US-10-170-385-389
2	85	90.4	193	16	US-10-723-860-529
3	57	60.6	126	10	US-09-764-891-4977
4	57	60.6	191	15	US-10-264-049-2611
5	47	50.0	620	15	US-10-369-493-14781
6	47	50.0	623	15	US-10-369-493-14935
7	47	50.0	649	15	US-10-369-493-11373
8	46	48.9	101	16	US-10-425-115-246626
9	46	48.9	211	15	US-10-225-066A-96
10	46	48.9	211	15	US-10-374-780A-2846
11	46	48.9	211	17	US-10-732-923-5447
					Sequence 389, App
					Sequence 529, App
					Sequence 4977, App
					Sequence 2611, App
					Sequence 14781, A
					Sequence 14935, A
					Sequence 11373, A
					Sequence 246626,
					Sequence 96, Appl
					Sequence 2846, App
					Sequence 5447, App

Query Match 90.4%; Score 85; DB 15; Length 193;

Best Local Similarity 93.8%; Pred. No. 4.7e-06; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

12	46	48.9	588	15	US-10-282-122A-77389	Sequence 77389, A
13	45	47.9	493	15	US-10-369-493-4327	Sequence 4327, App
14	45	47.9	493	15	US-10-369-493-7083	Sequence 7083, App
15	45	47.9	1411	15	US-10-282-122A-43060	Sequence 43060, A
16	44	46.8	74	16	US-10-437-963-110611	Sequence 110611,
17	44	46.8	90	16	US-10-425-115-350643	Sequence 350643,
18	44	46.8	108	16	US-10-425-115-351913	Sequence 351913,
19	44	46.8	131	17	US-10-935-098-99	Sequence 99, Appl
20	44	46.8	132	9	US-09-739-907-99	Sequence 99, Appl
21	44	46.8	132	11	US-09-938-671-99	Sequence 99, Appl
22	44	46.8	172	9	US-09-739-907-87	Sequence 87, Appl
23	44	46.8	172	11	US-09-938-671-87	Sequence 87, Appl
24	44	46.8	172	17	US-10-935-098-87	Sequence 87, Appl
25	44	46.8	177	11	US-09-833-245-1188	Sequence 1188, App
26	44	46.8	182	9	US-09-739-907-191	Sequence 191, App
27	44	46.8	182	11	US-09-938-671-191	Sequence 191, App
28	44	46.8	182	17	US-10-935-098-191	Sequence 191, App
29	44	46.8	213	16	US-10-425-115-224812	Sequence 224812,
30	44	46.8	330	11	US-09-833-245-1189	Sequence 1189, App
31	44	46.8	357	17	US-10-495-148-44	Sequence 44, Appl
32	44	46.8	406	9	US-09-731-872-245	Sequence 245, App
33	44	46.8	406	10	US-09-876-997-245	Sequence 245, App
34	44	46.8	406	11	US-09-978-360A-430	Sequence 430, App
35	44	46.8	406	14	US-10-028-072-66	Sequence 66, Appl
36	44	46.8	406	14	US-10-028-072-258	Sequence 258, App
37	44	46.8	406	14	US-10-140-808-66	Sequence 66, Appl
38	44	46.8	406	14	US-10-140-808-258	Sequence 258, App
39	44	46.8	406	14	US-10-121-049-66	Sequence 66, Appl
40	44	46.8	406	14	US-10-121-049-258	Sequence 258, App
41	44	46.8	406	14	US-10-123-904-66	Sequence 66, Appl
42	44	46.8	406	14	US-10-123-904-258	Sequence 258, App
43	44	46.8	406	14	US-10-140-470-66	Sequence 66, Appl
44	44	46.8	406	14	US-10-140-470-258	Sequence 258, App
45	44	46.8	406	14	US-10-175-746-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1

US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US2003020372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

Qy 1 FSWDNCPEGKDPVAVR 16
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Db 34 FSWDNCDEGKDPVAVR 49

RESULT 2

US-10-723-860-529
; Sequence 529, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 529
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-529

Query Match 90.4%; Score 85; DB 16; Length 193;
Best Local Similarity 93.8%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FSWDNCPEGKDPVAVR 16
|||||
Db 34 FSWDNCDEGKDPVAVR 49

RESULT 3

US-09-764-891-4977
; Sequence 4977, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764.891
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4977
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (119)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-4977

Query Match 60.6%; Score 57; DB 10; Length 126;
Best Local Similarity 50.0%; Pred. No. 0.16;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FSWDNCPEGKDPVAVR 16
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: : :

Db 52 FFWENCHERKDPVLLK 67

RESULT 4

US-10-264-049-2611
; Sequence 2611, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264.049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2611
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (141)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (142)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (184)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (187)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-2611

Query Match 60.6%; Score 57; DB 15; Length 191;
Best Local Similarity 50.0%; Pred. No. 0.24;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 FSWDNCPEGKDPVAVR 16
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Db 52 FFWENCHERKDPVLLK 67

RESULT 5

US-10-369-493-14781
; Sequence 14781, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14781
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:

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; NAME/KEY: unsure
; LOCATION: (1)..(620)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-14781

Query Match      50.0%; Score 47; DB 15; Length 620;
Best Local Similarity 56.2%; Pred. No. 40;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 2 SWDNCPEG--KDPAPI 15
Db 459 SWNNGFEGLTDDPAIV 474

RESULT 6
US-10-369-493-14935
; Sequence 14935, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14935
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(623)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-14935

Query Match      50.0%; Score 47; DB 15; Length 623;
Best Local Similarity 56.2%; Pred. No. 41;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 2 SWDNCPEG--KDPAPI 15
Db 458 SWNNGFEGLTDDPAIV 473

RESULT 7
US-10-369-493-11373
; Sequence 11373, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11373
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens

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US-10-369-493-11373

Query Match      50.0%; Score 47; DB 15; Length 649;
Best Local Similarity 56.2%; Pred. No. 42;
Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 2 SWDNCPEG--KDPAPI 15
Db 465 SWNNGFEGLTDDPAIV 480

RESULT 8
US-10-425-115-246626
; Sequence 246626, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 246626
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_156506C.1.pap
US-10-425-115-246626

Query Match      48.9%; Score 46; DB 16; Length 101;
Best Local Similarity 46.2%; Pred. No. 8;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 WDNCFEGKDPAPI 15
Db 28 WNSCFHGPEPPVM 40

RESULT 9
US-10-225-066A-96
; Sequence 96, Application US/10225066A
; Publication No. US20030226173A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J.
; APPLICANT: DUBELL, Arnold T.
; APPLICANT: HEARD, Jacqueline E.
; APPLICANT: PILGRIM, Marsha L.
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A.
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROWN, Pierre E.
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MB10036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11

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; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 211
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-96

Query Match 48.9%; Score 46; DB 15; Length 211;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SWDNCPEGKD 11
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Db 169 SWYNCDFGDD 178

RESULT 10
US-10-374-780A-2846
; Sequence 2846, Application US/10374780A
; Publication No. US2004001927A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Onaira
; APPLICANT: Yu, Guo-tiang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2846
; LENGTH: 211
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G2294
US-10-374-780A-2846

Query Match 48.9%; Score 46; DB 15; Length 211;
Best Local Similarity 70.0%; Pred. No. 19;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 SWDNCPEGKD 11
||| |||:|
Db 169 SWYNCDFGDD 178

RESULT 11
US-10-732-923-5447
; Sequence 5447, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 5447
; LENGTH: 211
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-10-732-923-5447

Query Match 48.9%; Score 46; DB 17; Length 211;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SWDNCPEGKD 11
||| |||:|
Db 169 SWYNCDFGDD 178

RESULT 12
US-10-282-122A-77389
; Sequence 77389, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

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; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77389
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77389

Query Match      48.9%; Score 46; DB 15; Length 588;
Best Local Similarity 57.1%; Pred. No. 56;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 WDNCFEGKDPVIR 16
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Db 447 WENSKGEDPVIK 460

RESULT 13
US-10-369-493-4327
; Sequence 4327, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4327
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4327

Query Match      47.9%; Score 45; DB 15; Length 493;
Best Local Similarity 58.3%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 WDNCFEGKDPV 14
   |||::|||
Db 449 WNCYQVMDPAV 460

RESULT 14
US-10-369-493-7083
; Sequence 7083, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7083
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; LENGTH: 493
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7083

Query Match      47.9%; Score 45; DB 15; Length 493;
Best Local Similarity 58.3%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 WDNCFEGKDPV 14
   |||::|||
Db 449 WNCYQVMDPAV 460

RESULT 15
US-10-282-122A-43060
; Sequence 43060, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43060
; LENGTH: 1411
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-282-122A-43060
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Query Match      47.9%; Score 45; DB 15; Length 1411;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 WDNCFEGKDPVIR 16
   |||::|||
Db 1354 WDEIFSGKDEKIVK 1367
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Search completed: July 27, 2005, 19:16:51
Job time : 36.0578 secs

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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:58:36 ; Search time 3.05778 Seconds
(without alignments)
390.606 Million cell updates/sec

Title: US-10-030-937-68

Perfect score: 16

Sequence: 1 FSWNCFEGKPAVIR 16

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	56.2	178	4	US-09-183-841-2
2	9	56.2	193	4	US-09-183-841-1
3	6	37.5	127	4	US-09-252-991A-18412
4	6	37.5	185	4	US-09-248-796A-16879
5	6	37.5	243	4	US-09-541-759-7
6	6	37.5	257	4	US-09-949-016-7490
7	6	37.5	297	1	US-08-534-9108-6
8	6	37.5	297	1	US-08-534-9108-7
9	6	37.5	297	1	US-08-534-9108-8
10	6	37.5	297	1	US-08-534-9108-9
11	6	37.5	297	3	US-08-534-9108-10
12	6	37.5	297	3	US-08-886-466-2
13	6	37.5	297	3	US-09-475-304-2
14	6	37.5	297	3	US-09-101-126-3
15	6	37.5	297	3	US-09-367-528A-1
16	6	37.5	297	3	US-09-367-528A-3
17	6	37.5	297	3	US-09-367-528A-5
18	6	37.5	1765	4	US-09-270-767-45587
19	5	31.2	25	1	US-07-706-699-1
20	5	31.2	25	1	US-07-998-931-1
21	5	31.2	25	4	US-09-042-460-52
22	5	31.2	30	3	US-08-851-843A-155
23	5	31.2	30	3	US-08-974-549A-275
24	5	31.2	30	3	US-08-854-050-155
25	5	31.2	30	3	US-09-430-323-155
26	5	31.2	30	4	US-09-402-181B-275
27	5	31.2	30	4	US-09-721-456-275

28 5 31.2 30 4 US-09-766-253-155 Sequence 155, App
29 5 31.2 35 2 US-08-737-716-12 Sequence 12, Appl
30 5 31.2 54 3 US-08-974-549A-25 Sequence 25, Appl
31 5 31.2 54 4 US-08-912-951-25 Sequence 25, Appl
32 5 31.2 54 4 US-09-402-181B-25 Sequence 25, Appl
33 5 31.2 54 4 US-09-721-456-25 Sequence 25, Appl
34 5 31.2 64 4 US-09-205-258-774 Sequence 774, App
35 5 31.2 73 4 US-09-438-185A-1008 Sequence 1008, App
36 5 31.2 78 4 US-09-489-039A-11104 Sequence 11104, A
37 5 31.2 82 4 US-09-198-452A-1142 Sequence 1142, A
38 5 31.2 82 4 US-09-270-767-58568 Sequence 58568, A
39 5 31.2 82 4 US-09-513-999C-5870 Sequence 5870, App
40 5 31.2 107 4 US-09-489-039A-11962 Sequence 11962, A
41 5 31.2 127 4 US-09-270-767-47503 Sequence 47503, A
42 5 31.2 145 4 US-09-270-767-43226 Sequence 43226, A
43 5 31.2 149 4 US-09-270-767-40911 Sequence 40911, A
44 5 31.2 149 4 US-09-270-767-56127 Sequence 56127, A
45 5 31.2 158 4 US-09-107-433-3844 Sequence 3844, App

ALIGNMENTS

RESULT 1

US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match 56.2%; Score 9; DB 4; Length 178;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPVIR 16
|||||
Db 26 EGKDPVIR 34

RESULT 2

US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

; LOCATION: (33)..(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1

Query Match 56.2%; Score 9; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDPVIR 16
|||||
DB 41 EGKDPVIR 49

RESULT 3
US-09-252-991A-18412
; Sequence 18412, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18412
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18412

Query Match 37.5%; Score 6; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDP A 13
|||||
DB 4 EGKDP A 9

RESULT 4
US-09-248-796A-16879
; Sequence 16879, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16879
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16879

Query Match 37.5%; Score 6; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KDPVIR 15

DB 171 KDPVIR 176
|||||

RESULT 5
US-09-541-759-7
; Sequence 7, Application US/09541759
; Patent No. 6723322
; GENERAL INFORMATION:
; APPLICANT: Lustigman, Sara
; APPLICANT: Pearlman, Eric
; APPLICANT: Unnaesch, Thomas
; TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
; FILE REFERENCE: 63475/252
; CURRENT APPLICATION NUMBER: US/09/541.759
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-541-759-7

Query Match 37.5%; Score 6; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDP A 13
|||||
DB 20 EGKDP A 25

RESULT 6
US-09-949-016-7490
; Sequence 7490, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7490
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7490

Query Match 37.5%; Score 6; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGKDP A 13
|||||
DB 34 EGKDP A 39

RESULT 7
US-08-534-910B-6
; Sequence 6, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi

```
;
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetoshi
; TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable
; TITLE OF INVENTION: Of Synthesizing Geranylgeranyldiphosphate And Gene Coding Ther
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; FILING DATE: 28-SEPT-1995
; APPLICATION NUMBER: US/08/534,910B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
; US-08-534-910B-6

Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
DB 62 GKDPV 67

RESULT 8
US-08-534-910B-7
; Sequence 7, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetoshi
; TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable
; TITLE OF INVENTION: Of Synthesizing Geranylgeranyldiphosphate And Gene Coding Ther
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
```

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;
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; FILING DATE: 28-SEPT-1995
; APPLICATION NUMBER: US/08/534,910B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
; US-08-534-910B-7

Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
DB 62 GKDPV 67

RESULT 9
US-08-534-910B-8
; Sequence 8, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetoshi
; TITLE OF INVENTION: Mutated Farnesylphosphate Synthase Capable
; TITLE OF INVENTION: Of Synthesizing Geranylgeranyldiphosphate And Gene Coding Ther
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; FILING DATE: 28-SEPT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
; US-08-534-910B-8

Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GKDPV 14
Db 62 GKDPV 67

RESULT 10
US-08-534-910B-9
; Sequence 9, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetoshi
; TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
; OF SYNTHESIZING GERANYLGERANYLDIPHOSPHATE AND GENE CODING THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,910B
; FILING DATE: 28-SEPT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
; US-08-534-910B-9

Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GKDPV 14
Db 62 GKDPV 67

RESULT 11
US-08-534-910B-10
; Sequence 10, Application US/08534910B
; Patent No. 5766911
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Ayumi
; APPLICANT: OBATA, Shusei
; APPLICANT: NISHINO, Tokuzo
; APPLICANT: OHNUMA, Shinichi
; APPLICANT: NAKAZAWA, Takeshi
; APPLICANT: OGURA, Kyoza
; APPLICANT: KOYAMA, Tanetoshi
; TITLE OF INVENTION: Mutated Farnesylidiphosphate Synthase Capable
; OF SYNTHESIZING GERANYLGERANYLDIPHOSPHATE AND GENE CODING THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: 1025 Connecticut Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.
; ZIP: 20036-5405
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.25" Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
; SOFTWARE: IBM/Word Perfect 6.1 Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/534,910B
; FILING DATE: 28-SEPT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-25253
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Toffenetti, Judith L.
; REGISTRATION NUMBER: 39,048
; REFERENCE/DOCKET NUMBER: 77670/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-1776
; TELEFAX: (202)429-0796
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus stearothermophilus
; US-08-534-910B-10

Query Match 37.5%; Score 6; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GKDPV 14
Db 62 GKDPV 67
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RESULT 12
US-08-886-466-2
; Sequence 2, Application US/08886466C
; Patent No. 6040165
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/08/886,466C
; CURRENT FILING DATE: 1997-07-10
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-08-886-466-2

Query Match 37.5%; Score 6; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
DB 62 GKDPV 67

RESULT 13
US-09-475-304-2
; Sequence 2, Application US/09475304
; Patent No. 6225096
; GENERAL INFORMATION:
; APPLICANT: Narita, Keishi
; APPLICANT: Ishida, Chika
; APPLICANT: Takeuchi, Yoshie
; APPLICANT: Ohto, Chikara
; APPLICANT: Ohnuma, Shinichi
; APPLICANT: Nishino, Tokuzo
; TITLE OF INVENTION: MUTANT PRENYL DIPHOSPHATE SYNTHASE
; FILE REFERENCE: 77670/494
; CURRENT APPLICATION NUMBER: US/09/475,304
; CURRENT FILING DATE: 1999-12-30
; EARLIER APPLICATION NUMBER: JP 8-191635
; EARLIER FILING DATE: 1996-07-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-475-304-2

Query Match 37.5%; Score 6; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
DB 62 GKDPV 67

RESULT 14
US-09-101-126-3
; Sequence 3, Application US/09101126

Patent No. 6316216
; GENERAL INFORMATION:
; APPLICANT: OHTO, CHIKARA
; APPLICANT: NAKANE, HIROYUKI
; APPLICANT: NISHINO, TOKUZO
; APPLICANT: OHNUMA, SHINICHI
; APPLICANT: HIROOKA, KAZUTAKE
; TITLE OF INVENTION: MUTATED PRENYL DIPHOSPHATE SYNTHASES
; FILE REFERENCE: 77670/566
; CURRENT APPLICATION NUMBER: US/09/101,126
; CURRENT FILING DATE: 1999-04-27
; EARLIER APPLICATION NUMBER: PCT/JP97/03921
; EARLIER FILING DATE: 1997-10-29
; EARLIER APPLICATION NUMBER: JP 8-307506
; EARLIER FILING DATE: 1996-11-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; OTHER INFORMATION: 86-92 is an Asp-rich domain
US-09-101-126-3

Query Match 37.5%; Score 6; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
DB 62 GKDPV 67

RESULT 15
US-09-367-528A-1
; Sequence 1, Application US/09367528A
; Patent No. 6395525
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; CURRENT FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: 82
; OTHER INFORMATION: Xaa represents Val, Leu, Ile, Thr, Asp, Glu, Asn, Gln, Lys,
; OTHER INFORMATION: Arg, Cys, Met, Phe, Tyr, Trp, His or Pro.
US-09-367-528A-1

Query Match 37.5%; Score 6; DB 3; Length 297;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKDPV 14
DB 62 GKDPV 67

Search completed: July 27, 2005, 19:17:42
Job time : 4.05778 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 19:08:40 ; Search time 8.88889 Seconds
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Title: US-10-030-937-68

Perfect score: 16

Sequence: 1 FSWNCFEGKDPVIR 16

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9	56.2	193	15	US-10-170-385-389
2	9	56.2	193	16	US-10-723-860-529
3	6	37.5	85	11	US-09-864-408A-5064
4	6	37.5	105	15	US-10-424-599-274901
5	6	37.5	126	9	US-09-815-242-5124
6	6	37.5	126	15	US-10-282-122A-43427
7	6	37.5	143	10	US-09-764-891-4060
8	6	37.5	160	15	US-10-424-599-260239
9	6	37.5	199	15	US-10-383-201-8
10	6	37.5	203	15	US-10-383-201-6
11	6	37.5	217	15	US-10-383-201-4
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					Sequence 529, Appli
					Sequence 5064, Ap
					Sequence 274901,
					Sequence 5124, Ap
					Sequence 43427, A
					Sequence 4060, Ap
					Sequence 260239,
					Sequence 8, Appli
					Sequence 6, Appli
					Sequence 4, Appli

12	6	37.5	243	15	US-10-383-201-2	Sequence 2, Appli
13	6	37.5	297	9	US-09-367-528A-1	Sequence 1, Appli
14	6	37.5	297	9	US-09-367-528A-3	Sequence 3, Appli
15	6	37.5	297	9	US-09-367-528A-5	Sequence 5, Appli
16	6	37.5	308	15	US-10-462-698A-76	Sequence 76, Appli
17	6	37.5	329	15	US-10-369-493-588	Sequence 52133, A
18	6	37.5	329	15	US-10-369-493-588	Sequence 588, App
19	6	37.5	329	17	US-10-732-923-5280	Sequence 5280, Ap
20	6	37.5	379	15	US-10-282-122A-60813	Sequence 60813, A
21	6	37.5	391	16	US-10-437-963-200217	Sequence 200217,
22	6	37.5	403	15	US-10-369-493-20145	Sequence 20145, A
23	6	37.5	423	18	US-10-637-831-6	Sequence 6, Appli
24	6	37.5	434	14	US-10-171-404A-46	Sequence 46, Appli
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26	6	37.5	446	15	US-10-282-122A-49297	Sequence 49297, A
27	6	37.5	471	16	US-10-437-963-203808	Sequence 203808,
28	6	37.5	474	17	US-10-732-923-1109	Sequence 1109, Ap
29	6	37.5	523	16	US-10-672-282-10	Sequence 10, Appli
30	6	37.5	526	16	US-10-672-282-3	Sequence 3, Appli
31	6	37.5	526	16	US-10-739-930-6665	Sequence 6665, Ap
32	6	37.5	641	16	US-10-437-963-137331	Sequence 137331,
33	6	37.5	757	16	US-10-437-963-185490	Sequence 185490,
34	6	37.5	825	16	US-10-408-765A-2285	Sequence 2285, Ap
35	6	37.5	912	16	US-10-623-813-7	Sequence 7, Appli
36	6	37.5	958	16	US-10-437-963-137333	Sequence 137333,
37	6	37.5	1036	16	US-10-437-963-126411	Sequence 126411,
38	6	37.5	1179	16	US-10-437-963-137323	Sequence 137323,
39	6	37.5	1191	16	US-10-437-963-126407	Sequence 126407,
40	6	37.5	1741	16	US-10-437-963-126375	Sequence 126375,
41	6	37.5	2112	15	US-10-437-963-126488	Sequence 126488,
42	6	37.5	3250	15	US-10-369-493-20151	Sequence 20151, A
43	5	31.2	13	15	US-10-468-370-631	Sequence 631, App
44	5	31.2	13	15	US-10-468-370-632	Sequence 632, App
45	5	31.2	13	15	US-10-468-370-633	Sequence 633, App

ALIGNMENTS

RESULT 1

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US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

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Query Match 56.2%; Score 9; DB 15; Length 193;
Best Local Similarity 100.0%; Pred.No. 0.062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 EGDPAVIR 16
Db      41 EGDPAVIR 49

RESULT 2
US-10-723-860-529
; Sequence 529, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 274901
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(105)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90256C.1.pep
US-10-424-599-274901

Query Match      37.5%; Score 6; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 59;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      8 EGDPA 13
Db      42 EGDPA 47

RESULT 5
US-09-815-242-5124
; Sequence 5124, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 5124
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

QY      11 DPAVIR 16
Db      73 DPAVIR 78

RESULT 4
US-09-864-408A-5064
; Sequence 5064, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9088
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5064
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-5064

Query Match      37.5%; Score 6; DB 11; Length 85;
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Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      11 DPAVIR 16
Db      73 DPAVIR 78

RESULT 4
US-10-723-860-529
; Sequence 529, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 529
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-529

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Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      8 EGDPAVIR 16
Db      41 EGDPAVIR 49
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US-09-815-242-5124

Query Match 37.5%; Score 6; DB 9; Length 126;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ECKDPA 13
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DB 3 ECKDPA 8

RESULT 6

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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
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; SOFTWARE: PatentIn version 3.1
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

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Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ECKDPA 13
|||||
DB 3 ECKDPA 8

RESULT 7

US-09-764-891-4060
; Sequence 4060, Application US/09764891

US-09-764-891-4060

Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4060
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (126)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (131)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-4060

Query Match 37.5%; Score 6; DB 10; Length 143;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ECKDPA 13
|||||
DB 76 ECKDPA 81

RESULT 8

US-10-424-599-260239
; Sequence 260239, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 260239
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT3847_77019C.1.pep
US-10-424-599-260239

Query Match 37.5%; Score 6; DB 15; Length 160;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 DPAVIR 16
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DB 99 DPAVIR 104

RESULT 9

US-10-383-201-8
; Sequence 8, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.

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; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 8
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-8

Query Match      37.5%; Score 6; DB 15; Length 199;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 EGKDP A 13
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Db      2 EGKDP A 7

RESULT 10
US-10-383-201-6
; Sequence 6, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-4

Query Match      37.5%; Score 6; DB 15; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 EGKDP A 13
        |||||
Db      20 EGKDP A 25

RESULT 12
US-10-383-201-2
; Sequence 2, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
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; SEQ ID NO 6
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-6

Query Match      37.5%; Score 6; DB 15; Length 203;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 EGKDP A 13
        |||||
Db      4 EGKDP A 9

RESULT 11
US-10-383-201-4
; Sequence 4, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 10/029020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/365,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,928
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-4

Query Match      37.5%; Score 6; DB 15; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 EGKDP A 13
        |||||
Db      20 EGKDP A 25

RESULT 12
US-10-383-201-2
; Sequence 2, Application US/10383201
; Publication No. US20040029226A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-568A
; CURRENT APPLICATION NUMBER: US/10/383,201
; CURRENT FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: CuraSeqList version 0.1
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; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/355,984
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/372,022
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/389,143
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/391,779
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/410,755
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 60/412,957
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 10/051,874
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/366,328
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/055,877
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 2
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-383-201-2

Query Match          37.5%; Score 6; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 EGKOPA 13
DB      20 EGKOPA 25
      |||||

RESULT 13
US-09-367-528A-1
; Sequence 1, Application US/09367528A
; Publication No. US20010051359A1
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: 82
; OTHER INFORMATION: Xaa represents Val, Leu, Ile, Thr, Asp, Glu, Asn, Gln, Lys,
; OTHER INFORMATION: Arg, Cys, Met, Phe, Tyr, Trp, His or Pro.
US-09-367-528A-1

Query Match          37.5%; Score 6; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GKDPV 14
DB      62 GKDPV 67
      |||||

RESULT 14
US-09-367-528A-3
; Sequence 3, Application US/09367528A
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; Publication No. US20010051359A1
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-367-528A-3

Query Match          37.5%; Score 6; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GKDPV 14
DB      62 GKDPV 67
      |||||

RESULT 15
US-09-367-528A-5
; Sequence 5, Application US/09367528A
; Publication No. US20010051359A1
; GENERAL INFORMATION:
; APPLICANT: TOYOTA JIDOSHA KABUSHIKI KAISHA
; TITLE OF INVENTION: Geranyl Diphosphate Synthetase Gene
; FILE REFERENCE: PH-586
; CURRENT APPLICATION NUMBER: US/09/367,528A
; PRIOR FILING DATE: 1999-08-16
; PRIOR APPLICATION NUMBER: JP97/346686
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
US-09-367-528A-5

Query Match          37.5%; Score 6; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GKDPV 14
DB      62 GKDPV 67
      |||||

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Job time : 8.88889 secs
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 19:16:56 ; Search time 42.4533 Seconds
(without alignments)
616.687 Million cell updates/sec

Title: US-10-030-937-68
Perfect score: 94
Sequence: 1 FSWNCFEGKDPVIR 16

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	53	56.4	35417	4	US-09-949-016-16129 Sequence 16129, A
c 2	53	56.4	49052	4	US-09-949-016-12203 Sequence 12203, A
c 3	51	54.3	561	4	US-09-489-039A-2692 Sequence 2692, Ap
4	50.5	53.7	45197	4	US-09-949-016-16208 Sequence 16208, A
5	50.5	53.7	254405	4	US-09-949-016-14381 Sequence 14381, A
c 6	49	52.1	240157	4	US-09-949-016-16284 Sequence 16284, A
7	48	51.1	4200	1	US-07-841-654B-1 Sequence 1, Appli
8	48	51.1	4200	1	US-07-946-234A-1 Sequence 1, Appli
9	48	51.1	4200	1	US-08-123-161A-1 Sequence 1, Appli
10	48	51.1	4200	1	US-08-483-278-1 Sequence 1, Appli
11	48	51.1	4200	5	PCT-US93-01560-1 Sequence 1, Appli
c 12	47	50.0	3647	4	US-09-949-016-2641 Sequence 2641, Ap

C	13	47	50.0	54950	4	US-09-949-016-14383	Sequence 14383, A
	14	46.5	49.5	12416	4	US-09-949-016-12000	Sequence 12000, A
	15	46.5	49.5	12418	4	US-09-949-016-16170	Sequence 16170, A
	C 16	46	48.9	6409	4	US-09-967-908A-1	Sequence 1, Appli
	C 17	46	48.9	6409	4	US-10-159-151-1	Sequence 1, Appli
	18	46	48.9	17644	4	US-09-949-016-16342	Sequence 16342, A
	19	46	48.9	17645	4	US-09-949-016-11805	Sequence 11805, A
	20	46	48.9	17645	4	US-09-949-016-14188	Sequence 14188, A
	21	46	48.9	44019	4	US-09-949-016-14902	Sequence 14902, A
C	22	46	48.9	640681	4	US-09-790-988-1	Sequence 1, Appli
	23	45	47.9	3940	4	US-09-976-594-573	Sequence 7, Appli
	24	45	47.9	28720	3	US-09-341-587-7	Sequence 7, Appli
	25	45	47.9	42975	4	US-09-949-016-11965	Sequence 11965, A
	26	45	47.9	115814	4	US-09-949-016-16205	Sequence 16205, A
	27	45	47.9	218940	4	US-09-949-016-17539	Sequence 17539, A
C	28	45	47.9	275110	4	US-09-949-016-12706	Sequence 12706, A
C	29	45	47.9	275110	4	US-09-949-016-16070	Sequence 16070, A
	30	45	47.9	1230025	4	US-09-198-452A-1	Sequence 1, Appli
	31	45	47.9	1230230	4	US-09-438-185A-1	Sequence 1, Appli
	32	44	46.8	601	4	US-09-949-016-25462	Sequence 25462, A
	33	44	46.8	601	4	US-09-949-016-25463	Sequence 25463, A
	34	44	46.8	601	4	US-09-949-016-25464	Sequence 25464, A
	35	44	46.8	601	4	US-09-949-016-25465	Sequence 25465, A
	36	44	46.8	601	4	US-09-949-016-25466	Sequence 25466, A
	37	44	46.8	601	4	US-09-949-016-48513	Sequence 48513, A
	38	44	46.8	601	4	US-09-949-016-73632	Sequence 73632, A
	39	44	46.8	601	4	US-09-949-016-73633	Sequence 73633, A
	40	44	46.8	601	4	US-09-949-016-73634	Sequence 73634, A
	41	44	46.8	601	4	US-09-949-016-73635	Sequence 73635, A
	42	44	46.8	601	4	US-09-949-016-73636	Sequence 73636, A
	43	44	46.8	1622	4	US-09-599-360B-48	Sequence 48, Appli
	44	44	46.8	3271	4	US-09-548-797B-1	Sequence 1, Appli
	45	44	46.8	3390	4	US-09-548-797B-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-16129/c
; Sequence 16129, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16129
; LENGTH: 35417
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16129

Alignment Scores:
Pred. No.: 200 Length: 35417
Score: 53.00 Matches: 9
Percent Similarity: 66.67% Conservative: 1
Best Local Similarity: 60.00% Mismatches: 5
Query Match: 56.38% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-68 (1-16) x US-09-949-016-16129 (1-35417)

QY 2 SerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16

ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: UIR89-11AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)861-6240
TELEFAX: (617)861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 170..2855
US-07-946-234A-1

Alignment Scores:
Pred. No.: 124 Length: 4200
Score: 48.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 51.06% Indels: 0
DB: 1 Gaps: 0

US-10-030-937-68 (1-16) x US-07-946-234A-1 (1-4200)

QY 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14
Db 73 TGGAGCAGGTGTGCAGAGGTGAGGACCGGCTCTG 108

RESULT 9

US-08-123-161A-1
Sequence 1, Application US/08123161A
Patent No. 5449616
GENERAL INFORMATION:
APPLICANT: Campbell, Kevin P.
APPLICANT: Roberts, Steven L.
APPLICANT: Anderson, Richard D.
APPLICANT: Ibraghimov, Oxana B.
APPLICANT: Yang, Bin
TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,161A
FILING DATE: 16-SEP-93
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/946,234
FILING DATE: 14-SEP-92
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: UIR89-11A4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 170..2855
US-08-123-161A-1
Alignment Scores:
Pred. No.: 124 Length: 4200
Score: 48.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 51.06% Indels: 0
DB: 1 Gaps: 0
US-10-030-937-68 (1-16) x US-08-123-161A-1 (1-4200)
QY 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14
Db 73 TGGAGCAGGTGTGCAGAGGTGAGGACCGGCTCTG 108
RESULT 10
US-08-483-278-1
Sequence 1, Application US/08483278
Patent No. 5686073
GENERAL INFORMATION:
APPLICANT: Campbell, Kevin P.
APPLICANT: Ibraghimov, Oxana B.
APPLICANT: Ervasti, James M.
APPLICANT: Levelle, Cynthia J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,278
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,161
FILING DATE: 16-SEP-93
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: UIR89-11A5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 170..2855

US-08-483-278-1

Alignment Scores: 124 Length: 4200
Pred. No.: 48.00 Matches: 7
Score: 75.00% Conservative: 2
Percent Similarity: 58.33% Mismatches: 3
Best Local Similarity: 51.06% Indels: 0
Query Match: 1 Gaps: 0
DB: 0

US-10-030-937-68 (1-16) x US-08-483-278-1 (1-4200)

Qy 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14
Db 73 TGGAGCAGGTGTGCAGAGGGTGAGGACCCGGCTCTG 108

RESULT 11

PCT-US93-01560-1
; Sequence 1. Application PC/TUS9301560
; GENERAL INFORMATION:
; APPLICANT: University of Iowa Research Foundation
; TITLE OF INVENTION: DNA ENCODING DYSTROPHIN-ASSOCIATED
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01560
; FILING DATE: 19930219
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/841,654
; FILING DATE: 20-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: UIRP89-11AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 861-6240
; TELEFAX: 617 861-9340
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4200 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 170..2855
PCT-US93-01560-1

Alignment Scores: 124 Length: 4200
Pred. No.: 48.00 Matches: 7
Score: 75.00% Conservative: 2
Percent Similarity: 58.33% Mismatches: 3
Best Local Similarity: 51.06% Indels: 0
Query Match: 5 Gaps: 0
DB: 0

US-10-030-937-68 (1-16) x PCT-US93-01560-1 (1-4200)

Qy 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14

Db 73 TGGAGCAGGTGTGCAGAGGGTGAGGACCCGGCTCTG 108

RESULT 12

US-09-949-016-2641/c
; Sequence 2641. Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2641
; LENGTH: 3647
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2641

Alignment Scores: 159 Length: 3647
Pred. No.: 47.00 Matches: 7
Score: 75.00% Conservative: 2
Percent Similarity: 58.33% Mismatches: 3
Best Local Similarity: 50.00% Indels: 0
Query Match: 4 Gaps: 0
DB: 0

US-10-030-937-68 (1-16) x US-09-949-016-2641 (1-3647)

Qy 3 TrpAspAsnCysPheGluGlyLysAspProAlaVal 14
Db 1836 TGGGATTGCTGTTTCCAGGGGAAAACCAATAGTG 1801

RESULT 13

US-09-949-016-14383/c
; Sequence 14383. Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14383
; LENGTH: 54950
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(54950)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14383

Alignment Scores: 4.4e+03 Length: 54950
Pred. No.: 4.4e+03

Score: 47.00 Matches: 7
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 58.33% Mismatches: 3
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-68 (1-16) x US-09-949-016-14383 (1-54950)

Qy 3 TrpAsnCysePheGluGlyLysAspProAlaVal 14
Db 51138 TGGGATTGCTGTTTCCAAAGGGGAAAAACCAATAGTG 51103

RESULT 14

US-09-949-016-12000
; Sequence 12000, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12000
; LENGTH: 12416
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12000

Alignment Scores:
Pred. No.: 882 Length: 12416
Score: 46.50 Matches: 9
Percent Similarity: 57.14% Conservative: 3
Best Local Similarity: 42.86% Mismatches: 4
Query Match: 49.47% Indels: 5
DB: 4 Gaps: 1

US-10-030-937-68 (1-16) x US-09-949-016-12000 (1-12416)

Qy 1 PheSerTrp-----AspAsnCysePheGluGlyLysAspProAlaVal 15
Db 4414 TTCTCTGGTCCAGTTTACCTTTAGATAAAATGTTTAAAGGGTAAAAATATGTGTATTCA 4473

Qy 16 Arg 16
Db 4474 AGA 4476

RESULT 15

US-09-949-016-16170
; Sequence 16170, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16170
; LENGTH: 12418
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16170

Alignment Scores:
Pred. No.: 883 Length: 12418
Score: 46.50 Matches: 9
Percent Similarity: 57.14% Conservative: 3
Best Local Similarity: 42.86% Mismatches: 4
Query Match: 49.47% Indels: 5
DB: 4 Gaps: 1

US-10-030-937-68 (1-16) x US-09-949-016-16170 (1-12418)

Qy 1 PheSerTrp-----AspAsnCysePheGluGlyLysAspProAlaVal 15
Db 4414 TTCTCTGGTCCAGTTTACCTTTAGATAAAATGTTTAAAGGGTAAAAATATGTGTATTCA 4473

Qy 16 Arg 16
Db 4474 AGA 4476

Search completed: July 27, 2005, 19:40:42
Job time : 66.4533 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 12:32:19 ; Search time 3.12889 Seconds
(without alignments)
381.728 Million cell updates/sec

Title: US-10-030-937-72

Perfect score: 83

Sequence: 1 YSLPKSEFAVPDLELP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	95.2	178	4	US-09-183-841-2
2	79	95.2	193	4	US-09-183-841-1
3	47	56.6	2710	2	US-08-568-459A-12
4	47	56.6	2710	2	US-08-487-826B-12
5	47	56.6	2710	3	US-09-210-288-12
6	47	56.6	3060	2	US-08-487-826B-14
7	44	53.0	307	4	US-09-543-681A-4241
8	43	51.8	471	3	US-08-911-853-4
9	43	51.8	471	3	US-09-479-409-4
10	43	51.8	471	3	US-09-479-453-4
11	43	51.8	812	4	US-09-489-039A-14282
12	41	49.4	74	4	US-09-902-540-11402
13	41	49.4	186	4	US-09-107-532A-5213
14	41	49.4	226	4	US-09-107-532A-6759
15	41	49.4	366	4	US-09-252-991A-26920
16	41	49.4	510	3	US-08-948-564-4
17	40.5	48.8	476	4	US-09-248-796A-20470
18	40	48.2	112	4	US-09-489-039A-14284
19	40	48.2	251	4	US-09-248-796A-19708
20	40	48.2	4536	4	US-09-180-422B-27
21	40	48.2	4536	4	US-09-079-030-1
22	40	48.2	4563	4	US-09-108-006C-1
23	40	48.2	4563	4	US-09-538-092-842
24	39.5	47.6	548	4	US-09-252-991A-21629
25	39	47.0	40	4	US-09-079-030-76
26	39	47.0	580	4	US-09-489-039A-14205
27	39	47.0	776	4	US-09-252-991A-17570

28 39 47.0 900 4 US-09-107-532A-5284 Sequence 5284, Ap
29 38.5 46.4 233 3 US-09-094-148-2 Sequence 2, Appli
30 38 45.8 22 4 US-09-079-030-79 Sequence 79, Appli
31 38 45.8 337 4 US-09-252-991A-16766 Sequence 16766, A
32 38 45.8 349 4 US-09-270-767-42023 Sequence 42023, A
33 38 45.8 421 4 US-09-198-452A-535 Sequence 535, App
34 38 45.8 423 4 US-09-248-796A-19425 Sequence 19425, A
35 38 45.8 429 4 US-09-438-185A-497 Sequence 437, App
36 38 45.8 433 4 US-09-538-092-1088 Sequence 1088, Ap
37 38 45.8 442 4 US-09-949-016-11671 Sequence 11671, A
38 38 45.8 537 3 US-08-886-886-17 Sequence 17, Appli
39 38 45.8 547 4 US-09-107-532A-5905 Sequence 5905, Ap
40 38 45.8 564 4 US-09-543-681A-6932 Sequence 6332, Ap
41 38 45.8 697 2 US-08-674-351-4 Sequence 4, Appli
42 38 45.8 840 4 US-09-079-030-214 Sequence 214, Appli
43 37.5 45.2 170 4 US-09-252-991A-29833 Sequence 29833, A
44 37.5 45.2 454 3 US-09-134-001C-4853 Sequence 4853, Ap
45 37.5 45.2 957 4 US-09-949-016-6154 Sequence 6154, Ap

ALIGNMENTS

RESULT 1

US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanx0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match 95.2%; Score 79; DB 4; Length 178;
Best Local Similarity 93.8%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSLPKSEFAVPDLELP 16
|||||
DB 130 YSLPKSEFAVPDLELP 145

RESULT 2

US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanx0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

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; LOCATION: (33)...(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1
  Query Match          95.2%; Score 79; DB 4; Length 193;
  Best Local Similarity 93.8%; Pred. No. 1.9e-06;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLELP 16
    ||||| |||||
Db 145 YSLPKSEFAVPDLELP 160

RESULT 3
US-08-568-459A-12
; Sequence 12, Application US/08568459A
; Patent No. 5849306
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
;
US-08-568-459A-12
  Query Match          56.6%; Score 47; DB 2; Length 2710;
  Best Local Similarity 64.3%; Pred. No. 28;
  Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LPKSEFAVPDLELP 16
    |||:: |||||
Db 2121 LPKNDGTVPDLEKP 2134

RESULT 4
US-08-487-826B-12
; Sequence 12, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2710 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium falciparum
;
US-08-487-826B-12
  Query Match          56.6%; Score 47; DB 2; Length 2710;
  Best Local Similarity 64.3%; Pred. No. 28;
  Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LPKSEFAVPDLELP 16
    |||:: |||||
Db 2121 LPKNDGTVPDLEKP 2134

RESULT 5
US-09-210-288-12
; Sequence 12, Application US/09210288
; Patent No. 6392026
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH121.1FWDV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-09-210-288-12

Query Match 56.6%; Score 47; DB 3; Length 2710;
Best Local Similarity 64.3%; Pred. No. 28;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LPKSEFAVPDLELP 16
||||:|||||
Db 2121 LPKNDGTVDPLEKP 2134

RESULT 6
US-08-487-826B-14
Sequence 14, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellem, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3060 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein,
US-08-487-826B-14

Query Match 56.6%; Score 47; DB 2; Length 3060;
Best Local Similarity 64.3%; Pred. No. 33;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LPKSEFAVPDLELP 16
||||:|||||
Db 2119 LPKNDGTVDPLEKP 2132

RESULT 7

US-09-543-681A-4241
Sequence 4241, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4241
LENGTH: 307
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-4241

Query Match 53.0%; Score 44; DB 4; Length 307;
Best Local Similarity 50.0%; Pred. No. 6.9;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 YSLPKSEFAVPDLE 14
||||:|||||
Db 220 YSLPQPQFTDPDIQ 233

RESULT 8

US-08-911-853-4
Sequence 4, Application US/08911853
Patent No. 6048710
GENERAL INFORMATION:
APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,853
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,092
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-911-853-4
Query Match 51.8%; Score 43; DB 3; Length 471;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLRLP 16
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Db 41 YSIPTDLVVSRLRLP 56

RESULT 9
US-09-479-409-4
; Sequence 4, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijabert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-479-409-4
Query Match 51.8%; Score 43; DB 3; Length 471;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLRLP 16
|||:|:|:|:|
Db 41 YSIPTDLVVSRLRLP 56

RESULT 9
US-09-479-409-4
; Sequence 4, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijabert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-479-409-4
Query Match 51.8%; Score 43; DB 3; Length 471;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLRLP 16
|||:|:~|:~|:~|
Db 41 YSIPTDLVVSRLRLP 56

RESULT 11
US-09-489-039A-14282
; Sequence 14282, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
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; TOPOLOGY: linear
;
US-09-479-409-4
Query Match 51.8%; Score 43; DB 3; Length 471;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLRLP 16
|||:~|:~|:~|
Db 41 YSIPTDLVVSRLRLP 56

RESULT 10
US-09-479-453-4
; Sequence 4, Application US/09479453
; Patent No. 6313283
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijabert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,453
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-479-453-4
Query Match 51.8%; Score 43; DB 3; Length 471;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLRLP 16
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Db 41 YSIPTDLVVSRLRLP 56

RESULT 11
US-09-489-039A-14282
; Sequence 14282, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
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; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14282
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-14282

Query Match          51.8%; Score 43; DB 4; Length 812;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 KSEFAVPDLELP 16
   |:|:|:|:|:|
Db 762 KADFRVPPLELP 773

RESULT 12
US-09-902-540-11402
; Sequence 11402, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10 (15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11402
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-11402

Query Match          49.4%; Score 41; DB 4; Length 74;
Best Local Similarity 43.8%; Pred. No. 4.2;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YSLPKSEFAVPDLELP 16
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Db 23 YRLPEAWAIPQLNP 38

RESULT 13
US-09-107-532A-5213
; Sequence 5213, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:

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; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6759:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 226 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
;   NAME/KEY: misc feature
;   LOCATION: (B) LOCATION 1...226
; SEQUENCE DESCRIPTION: SEQ ID NO: 6759:
US-09-107-532A-6759

Query Match      49.4%; Score 41; DB 4; Length 226;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      2 SLPKSEFAVPDL 13
Db      196 NLPSEAYIPDL 207
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RESULT 15
US-09-252-991A-26920
; Sequence 26920, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26920
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26920

Query Match      49.4%; Score 41; DB 4; Length 366;
Best Local Similarity 43.8%; Pred. No. 30;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy      1 YSLPKSEFAVPDLPLP 16
Db      186 YTIPEFDMVSDRLRP 201
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Job time : 4.12889 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:09:01 ; Search time 35.0578 Seconds

(without alignments)
177.532 Million cell updates/sec

Title: US-10-030-937-72

Perfect score: 83

Sequence: 1 YSLPKSEFAVPDLPLP 16

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Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	95.2	193	15	US-10-170-385-389 Sequence 389, App
2	79	95.2	193	16	US-10-723-860-529 Sequence 529, App
3	49	59.0	894	17	US-10-732-923-8428 Sequence 8428, App
4	47	56.6	2710	13	US-10-153-273-12 Sequence 12, Appl
5	44.5	53.6	120	15	US-10-424-599-284187 Sequence 284187, App
6	44	53.0	328	15	US-10-369-493-4173 Sequence 4173, App
7	44	53.0	329	15	US-10-320-797-3110 Sequence 3110, App
8	43.5	52.4	1383	14	US-10-021-955-82 Sequence 82, Appl
9	43.5	52.4	1383	14	US-10-021-955-86 Sequence 86, Appl
10	43.5	52.4	1383	14	US-10-021-955-87 Sequence 87, Appl
11	43.5	52.4	1389	14	US-10-021-955-79 Sequence 79, Appl

ALIGNMENTS

RESULT 1

US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US2003020372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

Query Match 95.2%; Score 79; DB 15; Length 193;
Best Local Similarity 93.8%; Pred. No. 5e-05; 1; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

12 43 51.8 183 16 US-10-425-115-261209 Sequence 261209,
13 43 51.8 828 15 US-10-282-122A-60144 Sequence 60144, A
14 42.5 51.2 104 16 US-10-425-115-194142 Sequence 194142,
15 42.5 51.2 1391 14 US-10-021-955-85 Sequence 85, Appl
16 42.5 51.2 1398 16 US-10-408-765A-1007 Sequence 1007, Ap
17 42.5 51.2 1461 10 US-09-940-227-77 Sequence 77, Appl
18 42.5 51.2 1461 14 US-10-021-955-88 Sequence 88, Appl
19 42.5 51.2 1461 15 US-10-467-433-10 Sequence 10, Appl
20 42.5 51.2 1461 15 US-10-332-947-30 Sequence 30, Appl
21 42.5 51.2 1461 17 US-10-933-058-77 Sequence 77, Appl
22 42.5 51.2 1483 15 US-10-332-947-29 Sequence 29, Appl
23 42.5 51.2 1549 15 US-10-363-616-314 Sequence 314, App
24 42 50.6 63 16 US-10-425-115-232729 Sequence 232729,
25 42 50.6 140 16 US-10-425-115-208031 Sequence 208031,
26 42 50.6 188 11 US-09-801-944B-234 Sequence 234, App
27 42 50.6 199 15 US-10-282-122A-65806 Sequence 65806, A
28 42 50.6 300 15 US-10-425-114-69294 Sequence 69294, A
29 42 50.6 393 15 US-10-282-122A-55243 Sequence 55243, A
30 42 50.6 852 16 US-10-437-963-204585 Sequence 204585,
31 42 50.6 1040 16 US-10-437-963-140470 Sequence 140470,
32 42 50.6 1127 16 US-10-437-963-140467 Sequence 140467,
33 42 50.6 1441 17 US-10-732-923-1652 Sequence 1652, Ap
34 42 50.6 1441 17 US-10-732-923-1653 Sequence 1653, Ap
35 41.5 50.0 186 15 US-10-425-114-39728 Sequence 39728, A
36 41.5 50.0 313 15 US-10-424-599-235166 Sequence 235166,
37 41 49.4 68 16 US-10-437-963-136391 Sequence 136391,
38 41 49.4 85 16 US-10-425-115-356159 Sequence 356159,
39 41 49.4 102 16 US-10-437-963-107307 Sequence 107307,
40 41 49.4 106 16 US-10-425-115-321334 Sequence 321334,
41 41 49.4 153 15 US-10-425-114-61811 Sequence 61811, A
42 41 49.4 159 16 US-10-425-115-224622 Sequence 224622,
43 41 49.4 187 16 US-10-425-115-208030 Sequence 208030,
44 41 49.4 267 16 US-10-425-115-208027 Sequence 208027,
45 41 49.4 337 15 US-10-369-493-19438 Sequence 19438, A

QY 1 YSLPKSEFAVPDLELP 16
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 Db 145 YSLPKSEFVVDLELP 160

RESULT 2

US-10-723-860-529
 ; Sequence 529, Application US/10723860
 ; Publication No. US20040253606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsburg, Wendy M.
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
 ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
 ; FILE REFERENCE: 05882.0193.NPUS01
 ; CURRENT APPLICATION NUMBER: US/10/723,860
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: 60/429,739
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 8393
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 529
 ; LENGTH: 193
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-723-860-529

Query Match 95.2%; Score 79; DB 16; Length 193;
 Best Local Similarity 93.8%; Pred. No. 5e-05;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YSLPKSEFAVPDLELP 16
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 Db 145 YSLPKSEFVVDLELP 160

RESULT 3

US-10-732-923-8428
 ; Sequence 8428, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 8428
 ; LENGTH: 894
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa (japonica cultivar-group)
 US-10-732-923-8428

Query Match 59.0%; Score 49; DB 17; Length 894;
 Best Local Similarity 61.5%; Pred. No. 30;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 LPKSEFAVPDLEL 15
 :||:|
 Db 817 VPRSEISPDLEL 829

RESULT 4

US-10-153-273-12
 ; Sequence 12, Application US/10153273
 ; Publication No. US20020169305A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Kim L.
 ; APPLICANT: Chitnis, Chetan

Miller, Louis H.
 Peterson, David S.
 Su, Xin-zhaun
 Wellem, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/10/153,273
 FILING DATE: 21-May-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/210,289
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Fuller, Michael
 REGISTRATION NUMBER: 36,516
 REFERENCE/DOCKET NUMBER: NIH21.1FWDV1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2710 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmodium falciparum
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 US-10-153-273-12
 Query Match 56.8%; Score 47; DB 13; Length 2710;
 Best Local Similarity 64.3%; Pred. No. 2.3e+02;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 3 LPKSEFAVPDLELP 16
 |||:|
 Db 2121 LPKNDGTVPDLEKP 2134
 RESULT 5
 US-10-424-599-284187
 ; Sequence 284187, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 284187
 ; LENGTH: 120
 ; TYPE: PRT

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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_98646C.1.pep
US-10-424-599-284187

Query Match      53.0%; Score 44.5; DB 15; Length 120;
Best Local Similarity 68.8%; Pred. No. 17;
Matches 11; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY      1 YSLPKSEFAVPDLELP 16
Db      98 YFLPLSE-SRPDLELP 112

RESULT 6
US-10-369-493-4173
; Sequence 4173, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4173
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(328)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-4173

Query Match      53.0%; Score 44; DB 15; Length 328;
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      4 PKSEFAVPDLELP 16
Db      105 PKAEWVPTLSLP 117

RESULT 7
US-10-320-797-3110
; Sequence 3110, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M.
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3110
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3110

Query Match      53.0%; Score 44; DB 15; Length 329;
Best Local Similarity 56.2%; Pred. No. 65;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 YSLPKSEFAVPDLELP 16
Db      58 FSLPVKFEQIIDLFLP 73

RESULT 8
US-10-021-955-82
; Sequence 82, Application US/10021955
; Publication No. US20030039987A1
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R
; APPLICANT: Boerkoel, Cornelius F
; APPLICANT: Takashima, Hiroshi
; TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
; FILE REFERENCE: P02086USI/10026309
; CURRENT APPLICATION NUMBER: US/10/021,955
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: US 60/255,217
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1383
; TYPE: PRT
; ORGANISM: Rat
US-10-021-955-82

Query Match      52.4%; Score 43.5; DB 14; Length 1383;
Best Local Similarity 60.0%; Pred. No. 46+02;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY      3 LPKS-EFAVPDLELP 16
Db      453 LKPAEAAIPDVQLP 467

RESULT 9
US-10-021-955-86
; Sequence 86, Application US/10021955
; Publication No. US20030039987A1
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R
; APPLICANT: Boerkoel, Cornelius F
; APPLICANT: Takashima, Hiroshi
; TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
; FILE REFERENCE: P02086USI/10026309
; CURRENT APPLICATION NUMBER: US/10/021,955
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: US 60/255,217
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 1383
; TYPE: PRT
; ORGANISM: Rat
US-10-021-955-86

Query Match      52.4%; Score 43.5; DB 14; Length 1383;
Best Local Similarity 60.0%; Pred. No. 46+02;
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY      3 LPKS-EFAVPDLELP 16
Db      453 LKPAEAAIPDVQLP 467

RESULT 10
US-10-021-955-87
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QY 5 KSEFVDPDLELP 16
|::|||
Db 758 KADFRVPPLELP 769

RESULT 14
US-10-425-115-194142
; Sequence 194142, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 194142
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_108637C.1.pep
US-10-425-115-194142

Query Match: 51.2%; Score 42.5; DB 16; Length 104;
Best Local Similarity 38.1%; Pred. No. 31;
Matches 8; Conservative 5; Mismatches 3; Indels 5; Gaps 1;

QY 1 YSLPKSEFA-----VPDLELP 16
:|::|||
Db 64 FEIPSEYSHNTIIVDPFEIP 84

RESULT 15
US-10-021-955-85
; Sequence 85, Application US/10021955
; Publication No. US20030039987A1
; GENERAL INFORMATION:
; APPLICANT: Lupeki, James R
; APPLICANT: Boerkoel, Cornelius F
; APPLICANT: Takashima, Hiroshi
; TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
; FILE REFERENCE: P02086US/10026309
; CURRENT APPLICATION NUMBER: US/10/021,955
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: US 60/255,217
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 1391
; TYPE: PRT
; ORGANISM: Mouse
US-10-021-955-85

Query Match: 51.2%; Score 42.5; DB 14; Length 1391;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 3 LPK-SSEFVDPDLELP 16
||| |
Db 510 LPKPEWAVDPVHLP 524

Search completed: July 27, 2005, 19:16:51
Job time : 35.0578 secs

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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:58:36 ; Search time 3.05778 Seconds
(without alignments)
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Title: US-10-030-937-72
Perfect score: 16
Sequence: 1 YSLPKSEFAVPDLELP 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	50.0	178	4	US-09-183-841-2
2	8	50.0	193	4	US-09-183-841-1
3	6	37.5	55	4	US-09-270-767-62426
4	6	37.5	112	4	US-09-489-039A-14284
5	6	37.5	219	4	US-09-248-796A-16515
6	6	37.5	223	4	US-09-543-681A-7057
7	6	37.5	223	4	US-09-583-110-3681
8	6	37.5	255	4	US-08-778-717-11
9	6	37.5	257	4	US-08-778-717-13
10	6	37.5	258	4	US-09-543-681A-8135
11	6	37.5	284	4	US-09-107-433-4311
12	6	37.5	309	4	US-09-302-540-13383
13	6	37.5	328	4	US-09-719-108-6
14	6	37.5	349	4	US-09-270-767-42023
15	6	37.5	356	4	US-09-270-767-46804
16	6	37.5	473	4	US-09-252-991A-23441
17	6	37.5	534	4	US-09-134-000C-5087
18	6	37.5	537	3	US-08-886-886-17
19	6	37.5	547	4	US-09-107-532A-5905
20	6	37.5	580	4	US-09-489-039A-14205
21	6	37.5	834	4	US-09-252-991A-17616
22	6	37.5	2329	3	US-08-755-587-16
23	6	37.5	2451	4	US-09-949-016-9675
24	6	37.5	2618	3	US-09-413-814-28
25	6	37.5	3418	2	US-08-639-501-2
26	6	37.5	3418	2	US-08-603-753D-4
27	6	37.5	3418	3	US-09-044-946-2

28	6	37.5	3418	3	US-08-755-587-44	Sequence 44, Appl
29	6	37.5	3418	3	US-09-044-908-2	Sequence 2, Appl
30	6	37.5	3418	3	US-09-099-753-4	Sequence 4, Appl
31	6	37.5	3418	3	US-08-986-106-4	Sequence 4, Appl
32	5	31.2	6	1	US-08-467-607-12	Sequence 12, Appl
33	5	31.2	6	2	US-08-469-362-12	Sequence 12, Appl
34	5	31.2	6	2	US-08-850-392-12	Sequence 12, Appl
35	5	31.2	11	3	US-09-476-482-11	Sequence 11, Appl
36	5	31.2	15	3	US-08-946-026-57	Sequence 5, Appl
37	5	31.2	19	2	US-08-793-490-5	Sequence 4, Appl
38	5	31.2	20	1	US-08-467-607-4	Sequence 4, Appl
39	5	31.2	20	2	US-08-469-362-4	Sequence 4, Appl
40	5	31.2	20	2	US-08-850-392-4	Sequence 4, Appl
41	5	31.2	21	3	US-09-406-781-40	Sequence 40, Appl
42	5	31.2	21	4	US-09-880-132-40	Sequence 40, Appl
43	5	31.2	35	3	US-09-079-372-11	Sequence 11, Appl
44	5	31.2	48	4	US-09-205-258-574	Sequence 574, Appl
45	5	31.2	54	4	US-09-640-211A-2293	Sequence 2293, Ap

ALIGNMENTS

RESULT 1
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match	50.0%;	Score 8;	DB 4;	Length 178;
Best Local Similarity	100.0%;	Pred. No. 0.35;		
Matches	8;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	1	YSLPKSEF 8		
Db	130	YSLPKSEF 137		

RESULT 2
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL

```
; LOCATION: (33)..(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1

Query Match      50.0%; Score 8; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSLPKSEF 8
Db 145 YSLPKSEF 152

RESULT 3
US-09-270-767-62426
; Sequence 62426, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62426
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-62426

Query Match      37.5%; Score 6; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SLPKSE 7
Db 32 SLPKSE 37

RESULT 4
US-09-489-039A-14284
; Sequence 14284, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14284
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14284

Query Match      37.5%; Score 6; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 FAVPDL 13
Db 107 FAVPDL 112
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```
RESULT 5
US-09-248-796A-16515
; Sequence 16515, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16515
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16515

Query Match      37.5%; Score 6; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KSEFAV 10
Db 207 KSEFAV 212

RESULT 6
US-09-543-681A-7057
; Sequence 7057, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7057
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7057

Query Match      37.5%; Score 6; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EFAVPD 12
Db 117 EFAVPD 122

RESULT 7
US-09-583-110-3681
; Sequence 3681, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
```


; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3681
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-583-110-3681

Query Match 37.5%; Score 6; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KSEFAV 10
DB 43 KSEFAV 48

RESULT 8

US-08-778-717-11
; Sequence 11, Application US/08778717
; Patent No. 6602689
; GENERAL INFORMATION:
; APPLICANT: UENO, EIICHI
; APPLICANT: NOBUYUKI, FUJII
; APPLICANT: OKADA, MASAHISA
; TITLE OF INVENTION: FUSED DNA SEQUENCE, FUSED PROTEIN
; TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
; TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778, 717
FILING DATE: 12-DEC-1996
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 352225/1995
FILING DATE: 28-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2084-031-0
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: RECOMBINANT
AUTHORS: NOBUYUKI FUJII ET AL,
TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF

EXPRESSING SAID FUSED PROTEIN

; RELEVANT RESIDUES IN SEQ ID NO: 11: FROM 1 TO 255
US-08-778-717-11

Query Match 37.5%; Score 6; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SEFAVP 11
DB 77 SEFAVP 82

RESULT 9

US-08-778-717-13
; Sequence 13, Application US/08778717
; Patent No. 6602689
; GENERAL INFORMATION:
; APPLICANT: UENO, EIICHI
; APPLICANT: NOBUYUKI, FUJII
; APPLICANT: OKADA, MASAHISA
; TITLE OF INVENTION: FUSED DNA SEQUENCE, FUSED PROTEIN
; TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
; TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778, 717
FILING DATE: 12-DEC-1996
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 352225/1995
FILING DATE: 28-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2084-031-0
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: RECOMBINANT
AUTHORS: NOBUYUKI FUJII ET AL,
TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF

EXPRESSING SAID FUSED PROTEIN
RELEVANT RESIDUES IN SEQ ID NO: 13: FROM 1 TO 257
US-08-778-717-13

Query Match 37.5%; Score 6; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SEFAVP 11


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; LENGTH: 329
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-719-108-6

Query Match      37.5%; Score 6; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SLPKSE 7
Db      66 SLPKSE 71

RESULT 14
US-09-270-767-42023
; Sequence 42023, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42023
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42023

Query Match      37.5%; Score 6; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PDLELP 16
Db      200 PDLELP 205

RESULT 15
US-09-270-767-46804
; Sequence 46804, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46804
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46804

Query Match      37.5%; Score 6; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 SLPKSE 7
Db      333 SLPKSE 338

Search completed: July 27, 2005, 19:17:43
Job time : 4.05778 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 19:08:40 ; Search time 8.8889 Seconds
(without alignments)
700.186 Million cell updates/sec

Title: US-10-030-937-72

Perfect score: 16

Sequence: 1 YSLPKSEPAVLDLPL 16

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Gapop 60.0 , Gapext 60.0

Searched: 1741741 seqs, 388992284 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	50.0	193	15 US-10-170-385-389	Sequence 389, App
2	8	50.0	193	16 US-10-723-860-529	Sequence 529, App
3	7	43.8	54	16 US-10-425-115-220040	Sequence 220040, App
4	6	37.5	39	11 US-09-833-245-1222	Sequence 1222, App
5	6	37.5	39	11 US-09-833-245-1224	Sequence 1224, App
6	6	37.5	51	16 US-10-437-963-105909	Sequence 105909, App
7	6	37.5	71	16 US-10-425-115-252984	Sequence 252984, App
8	6	37.5	86	16 US-10-437-963-188997	Sequence 188997, App
9	6	37.5	92	15 US-10-424-599-247004	Sequence 247004, App
10	6	37.5	95	9 US-09-925-299-1494	Sequence 1494, App
11	6	37.5	95	10 US-09-925-299-1494	Sequence 1494, App

12	6	37.5	101	15 US-10-282-122A-46052	Sequence 46052, A
13	6	37.5	116	15 US-10-424-599-188964	Sequence 188964, A
14	6	37.5	117	16 US-10-425-115-358214	Sequence 358214, A
15	6	37.5	120	15 US-10-424-599-284187	Sequence 284187, A
16	6	37.5	127	16 US-10-437-963-190106	Sequence 190106, A
17	6	37.5	129	16 US-10-437-963-133889	Sequence 133889, A
18	6	37.5	131	15 US-10-425-114-57104	Sequence 57104, A
19	6	37.5	151	9 US-09-738-626-4847	Sequence 4847, App
20	6	37.5	157	16 US-10-425-115-269204	Sequence 269204, A
21	6	37.5	158	17 US-10-732-923-21187	Sequence 21187, A
22	6	37.5	165	15 US-10-425-114-64412	Sequence 64412, A
23	6	37.5	176	14 US-10-168-066-6	Sequence 6, Appli
24	6	37.5	176	16 US-10-408-765A-1852	Sequence 1852, App
25	6	37.5	202	16 US-10-767-701-54502	Sequence 54502, A
26	6	37.5	214	9 US-09-999-602-1	Sequence 1, Appli
27	6	37.5	214	15 US-10-282-122A-69056	Sequence 69056, A
28	6	37.5	216	14 US-10-301-822-217	Sequence 217, App
29	6	37.5	216	15 US-10-425-114-50218	Sequence 50218, A
30	6	37.5	216	16 US-10-734-564-111	Sequence 111, App
31	6	37.5	220	17 US-10-732-923-21147	Sequence 21147, A
32	6	37.5	220	17 US-10-732-923-21391	Sequence 21391, A
33	6	37.5	227	16 US-10-425-115-255964	Sequence 255964, A
34	6	37.5	249	15 US-10-425-114-69119	Sequence 69119, A
35	6	37.5	251	14 US-10-301-822-220	Sequence 220, App
36	6	37.5	255	15 US-10-457-372-11	GENERAL INFORMA
37	6	37.5	257	14 US-10-106-698-6128	Sequence 6128, App
38	6	37.5	257	15 US-10-457-372-13	GENERAL INFORMA
39	6	37.5	267	14 US-10-301-822-215	Sequence 215, App
40	6	37.5	284	18 US-10-617-320-4311	Sequence 4311, App
41	6	37.5	295	15 US-10-425-114-37694	Sequence 37694, A
42	6	37.5	319	15 US-10-282-122A-50380	Sequence 50380, A
43	6	37.5	329	16 US-10-670-454-6	Sequence 6, Appli
44	6	37.5	330	15 US-10-155-435-10	Sequence 10, Appli
45	6	37.5	347	15 US-10-424-599-162707	Sequence 162707, A

ALIGNMENTS

RESULT 1
US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

Query Match 50.0%; Score 8; DB 15; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 YSLPKSEF 8
Db      145 YSLPKSEF 152

RESULT 2
US-10-723-860-529
; Sequence 529, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 529
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-529

Query Match      50.0%; Score 8; DB 16; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YSLPKSEF 8
Db      145 YSLPKSEF 152

RESULT 3
US-10-425-115-220040
; Sequence 220040, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 220040
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(54)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_132263C.1.pbp
US-10-425-115-220040

Query Match      43.8%; Score 7; DB 16; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 AVPDLEL 15
Db     10 AVPDLEL 16

us-10-030-937-72.oli.rapb

RESULT 4
US-09-833-245-1222
; Sequence 1222, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1222
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1222

Query Match      37.5%; Score 6; DB 11; Length 39;
Best Local Similarity 100.0%; Pred. No. 42;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 VPDLEL 15
Db       4 VPDLEL 9

RESULT 5
US-09-833-245-1224
; Sequence 1224, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1224
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1224

Query Match      37.5%; Score 6; DB 11; Length 39;
Best Local Similarity 100.0%; Pred. No. 42;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 VPDLEL 15
Db       4 VPDLEL 9

RESULT 6
US-10-437-963-105909
; Sequence 105909, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
```

; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105909
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10402C.1.pap
US-10-437-963-105909

Query Match 37.5%; Score 6; DB 16; Length 51;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSLPKS 6
DB 10 YSLPKS 15

RESULT 7
US-10-425-115-252984
; Sequence 252984, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 252984
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162304C.1.pap
US-10-425-115-252984

Query Match 37.5%; Score 6; DB 16; Length 71;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VPDLEL 15
DB 14 VPDLEL 19

RESULT 8
US-10-437-963-188997
; Sequence 188997, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 188997
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85548C.1.pap
US-10-437-963-188997

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Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FAVPDL 13
DB 45 FAVPDL 50

RESULT 9
US-10-424-599-247004
; Sequence 247004, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 247004
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_65074C.1.pap
US-10-424-599-247004

Query Match 37.5%; Score 6; DB 15; Length 92;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PDLELP 16
DB 43 PDLELP 48

RESULT 10
US-09-925-299-1494
; Sequence 1494, Application US/09925299
; Patent No. US2002005627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 1494
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (91)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (94)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-299-1494

Query Match 37.5%; Score 6; DB 9; Length 95;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PDLELP 16
Db 54 PDLELP 59

RESULT 11

US-09-925-299-1494
; Sequence 1494, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1494
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (91)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (93)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (94)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-299-1494

Query Match 37.5%; Score 6; DB 10; Length 95;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PDLELP 16
Db 54 PDLELP 59

RESULT 12

US-10-282-122A-46052
; Sequence 46052, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 46052

; LENGTH: 101

; TYPE: PRT

; ORGANISM: Bacillus anthracis

; US-10-282-122A-46052

Query Match 37.5%; Score 6; DB 15; Length 101;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SLPKSE 7

Db 13 SLPKSE 18

RESULT 13

US-10-424-599-188964
; Sequence 188964, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684


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; SEQ ID NO 188964
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_141649C.1.pap
US-10-424-599-188964

Query Match      37.5%; Score 6; DB 15; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 KSEFAV 10
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Db      86 KSEFAV 91

RESULT 14
US-10-425-115-358214
; Sequence 358214, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 358214
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(117)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_89859C.1.pap
US-10-425-115-358214

Query Match      37.5%; Score 6; DB 16; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PDLELP 16
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Db      18 PDLELP 23

RESULT 15
US-10-424-599-284187
; Sequence 284187, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 284187
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_98646C.1.pap
US-10-424-599-284187

Query Match      37.5%; Score 6; DB 15; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 PDLELP 16
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Db      107 PDLELP 112

Search completed: July 27, 2005, 19:27:29
Job time : 9.88889 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 19:16:56 ; Search time 42.4533 Seconds
(without alignments)
616.687 Million cell updates/sec

Title: US-10-030-937-72

Perfect score: 83

Sequence: 1 YSLPKSEFAVPDLPLP 16

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	56.6	8220	2	US-08-568-459A-11
2	47	56.6	8220	2	US-08-487-826B-11
3	47	56.6	8220	3	US-09-210-288-11
4	47	56.6	9280	4	US-08-956-171E-131
5	47	56.6	9280	4	US-08-781-986A-131
6	47	56.6	19124	2	US-08-487-826B-13
7	47	56.6	450395	4	US-09-949-016-15473
8	46	55.4	1062	4	US-09-894-844-61
9	46	55.4	4403765	3	US-09-103-840A-2
10	46	55.4	4403765	3	US-09-103-840A-2
11	46	55.4	4411529	3	US-09-103-840A-1
12	46	55.4	4411529	3	US-09-103-840A-1

13	44	53.0	924	4	US-09-543-681A-59	Sequence 69, Appl
14	44	53.0	17154	4	US-09-949-016-16889	Sequence 16889, A
15	44	53.0	31407	4	US-09-949-016-17359	Sequence 17359, A
16	44	53.0	46343	4	US-09-949-016-16824	Sequence 16824, A
17	44	53.0	64291	4	US-09-949-016-16278	Sequence 16278, A
18	44	53.0	117410	4	US-09-949-016-12262	Sequence 12262, A
19	43	51.8	601	4	US-09-949-016-20153	Sequence 20153, A
20	43	51.8	601	4	US-09-949-016-119374	Sequence 119374, A
21	43	51.8	1416	3	US-08-911-853-3	Sequence 3, Appl
22	43	51.8	1416	3	US-09-479-409-3	Sequence 3, Appl
23	43	51.8	1416	3	US-09-479-453-3	Sequence 3, Appl
24	43	51.8	2439	4	US-09-489-039A-7111	Sequence 7111, Ap
25	43	51.8	4377	3	US-08-911-853-28	Sequence 28, Appl
26	43	51.8	4377	3	US-09-479-403-28	Sequence 28, Appl
27	43	51.8	4377	3	US-09-479-453-28	Sequence 28, Appl
28	43	51.8	6308	4	US-09-949-016-12496	Sequence 12496, A
29	43	51.8	7144	4	US-09-949-016-14392	Sequence 14392, A
30	43	51.8	10086	4	US-09-949-016-15056	Sequence 15056, A
31	43	51.8	35064	4	US-09-949-016-12778	Sequence 12778, A
32	43	51.8	35065	4	US-09-949-016-13196	Sequence 13196, A
33	43	51.8	112132	3	US-09-741-150-3	Sequence 3, Appl
34	43	51.8	112132	4	US-10-160-187-3	Sequence 3, Appl
35	43	51.8	1830121	4	US-09-557-884-1	Sequence 1, Appl
36	43	51.8	1830121	4	US-09-643-990A-1	Sequence 1, Appl
37	42	50.6	354	4	US-09-513-999C-13536	Sequence 13536, A
38	42	50.6	601	4	US-09-949-016-87635	Sequence 87635, A
39	42	50.6	601	4	US-09-949-016-87636	Sequence 87636, A
40	42	50.6	601	4	US-09-949-016-87637	Sequence 87637, A
41	42	50.6	601	4	US-09-949-016-91953	Sequence 91953, A
42	42	50.6	601	4	US-09-949-016-91954	Sequence 91954, A
43	42	50.6	601	4	US-09-949-016-91955	Sequence 91955, A
44	42	50.6	1256	4	US-09-902-504-5454	Sequence 5454, Ap
45	42	50.6	1404	4	US-09-614-221A-277	Sequence 277, App

ALIGNMENTS

RESULT 1

US-08-568-459A-11
; Sequence 11, Application US/08568459A
; Patent No. 5849306

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX

TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESSES:

ADDRESSER: Knobbbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/568,459A

FILING DATE: 07-DEC-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Israel, Ned

REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH121.001CPI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX:	(619) 235-0176
INFORMATION FOR SEQ ID NO:	11:
SEQUENCE CHARACTERISTICS:	
LENGTH:	8220 base pairs
TYPE:	nucleic acid
STRANDEDNESS:	single
TOPOLOGY:	linear
MOLECULE TYPE:	DNA (genomic)
HYPOTHETICAL:	NO
ORIGINAL SOURCE:	
ORGANISM:	Plasmodium falciparum
US-08-568-459A-11	
Alignment Scores:	
Pred. No.:	228
Score:	47.00
Percent Similarity:	78.57%
Best Local Similarity:	64.29%
Query Match:	56.63%
DB:	2
Length:	8220
Matches:	9
Conservative:	2
Mismatches:	3
Indels:	0
Gaps:	0
US-10-030-937-72 (1-16) x US-08-568-459A-11 (1-8220)	
Qy	3 LeuProlySerGluPheAlaValProAspLeuGluLeuPro 16
Db	6341 CTTCCAAAAACGATGGAACCTGTTCCGGATTTAGAAAAGCCG 6382
RESULT 2	
US-08-487-826B-11	
Sequence 11, Application US/08487826B	
Patent No. 5993827	
GENERAL INFORMATION:	
APPLICANT:	Sim, Kim L.
APPLICANT:	Chitnis, Chetan
APPLICANT:	Miller, Louis H.
APPLICANT:	Peterson, David S.
APPLICANT:	Su, Xin-zhaun
APPLICANT:	Wellems, Thomas E.
TITLE OF INVENTION:	BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION:	AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES:	45
CORRESPONDENCE ADDRESS:	
ADDRESS:	Knobbe Martens Olson & Bear
STREET:	620 Newport Center Drive 16th Floor
CITY:	Newport Beach
STATE:	California
COUNTRY:	US
ZIP:	92660
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/487,826B
FILING DATE:	10-SEP-1993
CLASSIFICATION:	435
ATTORNEY/AGENT INFORMATION:	
NAME:	Israelsen, Ned
REGISTRATION NUMBER:	29,655
REFERENCE/DOCKET NUMBER:	NIH121.001CP1
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(619) 235-8550
TELEFAX:	(619) 235-0176
INFORMATION FOR SEQ ID NO:	11:
SEQUENCE CHARACTERISTICS:	
LENGTH:	8220 base pairs
TYPE:	nucleic acid
STRANDEDNESS:	single
TOPOLOGY:	linear
MOLECULE TYPE:	DNA (genomic)
HYPOTHETICAL:	NO
ORIGINAL SOURCE:	
ORGANISM:	Plasmodium falciparum
US-08-568-459A-11	
Alignment Scores:	
Pred. No.:	228
Score:	47.00
Percent Similarity:	78.57%
Best Local Similarity:	64.29%
Query Match:	56.63%
DB:	2
Length:	8220
Matches:	9
Conservative:	2
Mismatches:	3
Indels:	0
Gaps:	0
US-10-030-937-72 (1-16) x US-08-568-459A-11 (1-8220)	
Qy	3 LeuProlySerGluPheAlaValProAspLeuGluLeuPro 16
Db	6341 CTTCCAAAAACGATGGAACCTGTTCCGGATTTAGAAAAGCCG 6382
RESULT 2	
US-08-487-826B-11	
Sequence 11, Application US/08487826B	
Patent No. 5993827	
GENERAL INFORMATION:	
APPLICANT:	Sim, Kim L.
APPLICANT:	Chitnis, Chetan
APPLICANT:	Miller, Louis H.
APPLICANT:	Peterson, David S.
APPLICANT:	Su, Xin-zhaun
APPLICANT:	Wellems, Thomas E.
TITLE OF INVENTION:	BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION:	AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES:	45
CORRESPONDENCE ADDRESS:	
ADDRESS:	Knobbe Martens Olson & Bear
STREET:	620 Newport Center Drive 16th Floor
CITY:	Newport Beach
STATE:	California
COUNTRY:	US
ZIP:	92660
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/08/487,826B
FILING DATE:	10-SEP-1993
CLASSIFICATION:	435
ATTORNEY/AGENT INFORMATION:	
NAME:	Israelsen, Ned
REGISTRATION NUMBER:	29,655
REFERENCE/DOCKET NUMBER:	NIH121.001CP1
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(619) 235-8550
TELEFAX:	(619) 235-0176
INFORMATION FOR SEQ ID NO:	11:
SEQUENCE CHARACTERISTICS:	
LENGTH:	8220 base pairs
TYPE:	nucleic acid
STRANDEDNESS:	single
TOPOLOGY:	linear
MOLECULE TYPE:	DNA (genomic)
HYPOTHETICAL:	NO
ORIGINAL SOURCE:	
ORGANISM:	Plasmodium falciparum
US-08-568-459A-11	
Alignment Scores:	
Pred. No.:	228
Score:	47.00
Percent Similarity:	78.57%
Best Local Similarity:	64.29%
Query Match:	56.63%
DB:	2
Length:	8220
Matches:	9
Conservative:	2
Mismatches:	3
Indels:	0
Gaps:	0
US-10-030-937-72 (1-16) x US-08-487-826B-11 (1-8220)	
Qy	3 LeuProlySerGluPheAlaValProAspLeuGluLeuPro 16
Db	6341 CTTCCAAAAACGATGGAACCTGTTCCGGATTTAGAAAAGCCG 6382
RESULT 3	
US-09-210-288-11	
Sequence 11, Application US/09210288	
Patent No. 6392026	
GENERAL INFORMATION:	
APPLICANT:	Sim, Kim L.
APPLICANT:	Chitnis, Chetan
APPLICANT:	Miller, Louis H.

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US-10-030-937-72 (1-16) x US-09-210-288-11 (1-8220)
; Sequence 131, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-131

Alignment Scores:
Pred. No.: 265 Length: 9280
Score: 47.00 Matches: 8
Percent Similarity: 86.67% Conservative: 5
Best Local Similarity: 53.33% Mismatches: 2
Query Match: 56.63% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-08-781-986A-131 (1-9280)
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Db 6399 ACGTTCGGAATCAAAGTTGCTTTACCAACCAATATTCATACCA 6443

RESULT 6
US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellem, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California

US-10-030-937-72 (1-16) x US-09-210-288-11 (1-8220)
; Sequence 131, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 131:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9280 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-956-171E-131

Alignment Scores:
Pred. No.: 265 Length: 9280
Score: 47.00 Matches: 8
Percent Similarity: 86.67% Conservative: 5
Best Local Similarity: 53.33% Mismatches: 2
Query Match: 56.63% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-08-956-171E-131 (1-9280)
QY 2 SerLeuProLySerGluPheAlaValProAspLeuGluLeuPro 16
Db 6399 ACGTTCGGAATCAAAGTTGCTTTACCAACCAATATTCATACCA 6443

RESULT 5
US-08-781-986A-131
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; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-487-826B-13

Alignment Scores:
Pred. No.: 660 Length: 19124
Score: 47.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 56.63% Indels: 0
DB: 2 Gaps: 0

US-10-030-937-72 (1-16) x US-08-487-826B-13 (1-19124)

Qy 3 LeuProlysserGluPheAlaValProAspLeuGluLeuPro 16
Db 13661 CTTCCAAAACGATGGAAGTCTCCGGATTGAGAAAGCGG 13702

RESULT 7
US-09-949-016-15473/c
; Sequence 15473, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15473
; LENGTH: 450395
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(450395)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15473

Alignment Scores:
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Pred. No.: 3.53e+04 Length: 450395
Score: 47.00 Matches: 8
Percent Similarity: 84.62% Conservative: 3
Best Local Similarity: 61.54% Mismatches: 2
Query Match: 56.63% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-949-016-15473 (1-450395)

Qy 1 TyrSerLeuProlysserGluPheAlaValProAspLeu 13
Db 110299 TATAGCATGCCCAACTGAGTTCCTGGTTCCTCCCTC 110261

RESULT 8
US-09-894-844-61/c
; Sequence 61, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-61

Alignment Scores:
Pred. No.: 26.7 Length: 1062
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 55.42% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-894-844-61 (1-1062)

Qy 3 LeuProlysserGluPheAlaValProAspLeuGluLeuPro 16
Db 839 TTGCCGAAGCCCGAGTTCGATGATCCCGAGTTCGCACTGCCA 798

RESULT 9
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
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; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 8.05e+05 Length: 4403765
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 55.42% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-72 (1-16) x US-09-103-840A-2 (1-4403765)
QY 3 LeuProlyserGluPheAlaValProAspLeuGluLeuPro 16
Db 2632604 TTGCGGAGCCGAGTCTGTAATGCCGAGTTGCCACTGCCA 2632645

RESULT 10
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 8.05e+05 Length: 4403765
Score: 46.00 Matches: 8
Percent Similarity: 68.75% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 55.42% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-72 (1-16) x US-09-103-840A-2 (1-4403765)
QY 1 TyrSerLeuProlyserGluPheAlaValProAspLeuGluLeuPro 16
Db 299240 TACAGCGCACCGAAGCCGAGCGGCCACACCCGAGACGACCATCCCG 299193

RESULT 11
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1
Alignment Scores:
Pred. No.: 8.06e+05 Length: 4411529
Score: 46.00 Matches: 9
Percent Similarity: 78.57% Conservative: 2
Best Local Similarity: 64.29% Mismatches: 3
Query Match: 55.42% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-72 (1-16) x US-09-103-840A-1 (1-4411529)
QY 3 LeuProlyserGluPheAlaValProAspLeuGluLeuPro 16
Db 2634752 TTGCGGAGCCGAGTCTGTAATGCCGAGTTGCCACTGCCA 2634793

RESULT 12
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1

Alignment Scores:
Pred. No.: 8.06e+05 Length: 4411529
Score: 46.00 Matches: 8
Percent Similarity: 68.75% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 55.42% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-72 (1-16) x US-09-103-840A-1 (1-4411529)
QY 1 TyrSerLeuProlyserGluPheAlaValProAspLeuGluLeuPro 16
Db 299129 TACAGCGCACCGAAGCCGAGCGGCCACACCCGAGACGACCATCCCG 299082

RESULT 13
US-09-543-681A-69
; Sequence 69, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 69
; LENGTH: 924
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-69

Alignment Scores:
Pred. No.: 53.8 Length: 924
Score: 44.00 Matches: 7
Percent Similarity: 78.57% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 3
Query Match: 53.01% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-543-681A-69 (1-924)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGlu 14
Db 658 TACAGTTTACCTCAACCAATTCTACTGATCCGTATTCAA 699

RESULT 14

US-09-949-016-16889
; Sequence 16889, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16889
; LENGTH: 17154
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16889

Alignment Scores:
Pred. No.: 2.15e+03 Length: 17154
Score: 44.00 Matches: 9
Percent Similarity: 83.33% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 53.01% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-949-016-16889 (1-17154)

Qy 2 SerLeuProLysSerGluPheAlaValProAspLeu 13
Db 13244 TCCCTGCCAAAATCGCCCTTTGCCCTTCCCACTCTG 13279

RESULT 15

US-09-949-016-17359/C
; Sequence 17359, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17359
; LENGTH: 31407
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(31407)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17359

Alignment Scores:
Pred. No.: 4.6e+03 Length: 31407
Score: 44.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 53.01% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-72 (1-16) x US-09-949-016-17359 (1-31407)

Qy 7 GluPheAlaValProAspLeuGluLeu 15
Db 2930 GAATTGGCCATCCCTGATTAGAACTT 2904

Search completed: July 27, 2005, 19:54:20
Job time : 860.453 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Maximum Match 100%
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22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	79	95.2	448	11	US-09-969-034-4215 Sequence 4215, Ap
2	79	95.2	453	20	US-10-723-860-528 Sequence 528, App
3	79	95.2	1935	10	US-09-971-392-102 Sequence 102, App
4	79	95.2	2384	9	US-09-822-849A-53 Sequence 53, Appl
5	79	95.2	2436	9	US-09-954-531-380 Sequence 380, App
6	79	95.2	2436	20	US-09-525-978B-81 Sequence 81, Appl
7	79	95.2	2436	21	US-10-843-641A-1447 Sequence 1447, Ap
8	79	95.2	2478	17	US-10-170-385-390 Sequence 390, App
9	79	95.2	3988	20	US-10-723-860-5187 Sequence 5187, Ap
10	79	95.2	250000	16	US-10-225-810-26 Sequence 26, Appl
11	69	83.1	1983	17	US-10-388-934-167 Sequence 167, App
12	68	81.9	596	22	US-10-972-079-7219 Sequence 7219, Ap
13	68	81.9	599	22	US-10-972-079-7218 Sequence 7218, Ap
14	49	59.0	2269	19	US-10-437-963-4335 Sequence 4335, Ap
15	48	57.8	475	19	US-10-021-323-4461 Sequence 4461, Ap
16	48	57.8	475	19	US-10-767-795-2700 Sequence 2700, Ap
17	48	57.8	2796	19	US-10-437-963-97626 Sequence 97626, A
18	48	57.8	3335	19	US-10-437-963-97629 Sequence 97629, A
19	47	56.6	790	20	US-10-653-047-4552 Sequence 4552, Ap
20	47	56.6	3700	21	US-10-899-942-6 Sequence 6, Appl
21	47	56.6	8220	13	US-10-153-273-11 Sequence 11, Appl
22	47	56.6	9280	8	US-08-781-986A-131 Sequence 131, App
23	47	56.6	9280	18	US-10-329-650-131 Sequence 131, App
24	47	56.6	68233	17	US-10-034-650-31 Sequence 31, Appl
25	47	56.6	122614	13	US-10-087-192-1726 Sequence 1726, Ap
26	47	56.6	402850	13	US-09-844-653-5 Sequence 5, Appl
27	46	55.4	442	20	US-10-425-115-45305 Sequence 45305, A
28	46	55.4	535	17	US-10-027-632-24658 Sequence 24658, A
29	46	55.4	535	17	US-10-027-632-24658 Sequence 61, Appl
30	46	55.4	1062	9	US-09-894-844-61 Sequence 61, Appl
31	46	55.4	1062	17	US-10-388-902-61 Sequence 61, Appl
32	46	55.4	1062	15	US-10-647-089-61 Sequence 50, Appl
33	46	55.4	4999	18	US-10-225-486-50 Sequence 50, Appl
34	46	55.4	4999	20	US-10-723-860-3784 Sequence 3784, Ap
35	46	55.4	4999	21	US-10-651-237-57 Sequence 57, Appl
36	46	55.4	4999	21	US-10-782-413-57 Sequence 57, Appl
37	46	55.4	5755	20	US-10-723-860-7718 Sequence 7718, Ap
38	45	54.2	350	20	US-10-723-860-4061 Sequence 4061, Ap
39	45	54.2	626	20	US-10-357-930-53483 Sequence 53483, A
40	45	54.2	1200	17	US-10-282-122A-24975 Sequence 24975, A
41	45	54.2	1749	17	US-10-172-118-1397 Sequence 1397, Ap
42	45	54.2	1749	17	US-10-295-027-457 Sequence 457, App
43	45	54.2	1749	17	US-10-295-027-1095 Sequence 1095, Ap
44	45	54.2	1749	18	US-10-342-887-1397 Sequence 1397, Ap
45	45	54.2	1749	20	US-10-422-522-34 Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-969-034-4215
; Sequence 4215, Application US/09969034
; Publication No. US20040110668A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poorima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; TITLE OF INVENTION: Expressed in Cancer Tissue
; FILE REFERENCE: 1657/1032

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; CURRENT APPLICATION NUMBER: US/09/969,034
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4215
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 241, 277, 288, 295, 299, 300, 304, 310, 316, 343, 346, 356,
; LOCATION: 364, 370, 396, 397, 406, 410, 415, 424, 437
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-4215

Alignment Scores:
Pred. No.: 2.68e-05 Length: 448
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 11 Gaps: 0

US-10-030-937-72 (1-16) x US-09-969-034-4215 (1-448)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 43 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGACCTGGAGCTGCC 90

RESULT 2
US-10-723-860-528
; Sequence 528, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 528
; LENGTH: 953
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-528

Alignment Scores:
Pred. No.: 6.36e-05 Length: 953
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 20 Gaps: 0

US-10-030-937-72 (1-16) x US-10-723-860-528 (1-953)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 523 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGACCTGGAGCTGCC 570

RESULT 3
US-09-971-392-102
; Sequence 102, Application US/09971392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Peterson, David P.
; APPLICANT: Pearson, Cecelia I.
; APPLICANT: Pecks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: FA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 102
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Template ID: 977615.8
US-09-971-392-102

Alignment Scores:
Pred. No.: 0.000143 Length: 1935
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 10 Gaps: 0

US-10-030-937-72 (1-16) x US-09-971-392-102 (1-1935)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 534 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGACCTGGAGCTGCC 581

RESULT 4
US-09-822-849A-53
; Sequence 53, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-53

Alignment Scores:
Pred. No.: 0.000182 Length: 2384
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 9 Gaps: 0

US-10-030-937-72 (1-16) x US-09-822-849A-53 (1-2384)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
```

Db 445 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGACCTGAGCTGCC 492

RESULT 5

US-09-954-531-380
 ; Sequence 380, Application US/09954531
 ; Patent No. US20020165180A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weaver, Zoe
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
 ; FILE OF INVENTION: Gene Sets
 ; FILE REFERENCE: 689290-77
 ; CURRENT APPLICATION NUMBER: US/09/954,531
 ; CURRENT FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: US/60/233,133
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US/60/234,009
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: US/60/234,034
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: US/60/234,509
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: US/60/234,567
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 1392
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 380
 ; LENGTH: 2436
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-954-531-380

Alignment Scores: Length: 2436
 Pred. No.: 0.000187
 Score: 79.00 Matches: 15
 Percent Similarity: 93.75%
 Best Local Similarity: 93.75%
 Query Match: 95.18%
 Indels: 0
 Gaps: 0

US-10-030-937-72 (1-16) x US-09-954-531-380 (1-2436)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
 Db 491 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGACCTGAGCTGCC 538

RESULT 6

US-09-525-978B-81
 ; Sequence 81, Application US/09525978B
 ; Publication No. US20030049722A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Murray, Richard
 ; APPLICANT: Caras, Ingrid W.
 ; APPLICANT: Hevezi, Peter
 ; APPLICANT: Wilson, Keith
 ; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING MACROPHAGE DEVELOPMENT
 ; TITLE OF INVENTION: RELATED DISORDERS, COMPOSITIONS, AND METHODS OF
 ; TITLE OF INVENTION: SCREENING FOR MACROPHAGE DEVELOPMENT MODULATORS
 ; FILE REFERENCE: A-67413-1/DJB/JJD
 ; CURRENT APPLICATION NUMBER: US/09/525,978B
 ; CURRENT FILING DATE: 2000-03-15
 ; PRIOR APPLICATION NUMBER: USSN 60/124,530
 ; PRIOR FILING DATE: 1999-03-15
 ; NUMBER OF SEQ ID NOS: 83
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 81
 ; LENGTH: 2436
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-525-978B-81

Alignment Scores: Length: 2436
 Pred. No.: 0.000187

Score: 79.00 Matches: 15
 Percent Similarity: 93.75%
 Best Local Similarity: 93.75%
 Query Match: 95.18%
 Indels: 0
 Gaps: 0

US-10-030-937-72 (1-16) x US-09-525-978B-81 (1-2436)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
 Db 491 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGACCTGAGCTGCC 538

RESULT 7

US-10-843-641A-1447
 ; Sequence 1447, Application US/10843641A
 ; Publication No. US20050064454A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Avalon Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
 ; FILE OF INVENTION: Signature Gene Sets
 ; FILE REFERENCE: 689290-189
 ; CURRENT APPLICATION NUMBER: US/10/843,641A
 ; CURRENT FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: US/09/873,367
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US/09/954,531
 ; PRIOR FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: US/09/954,456
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US/09/962,436
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US/09/962,832
 ; PRIOR FILING DATE: 2001-09-25
 ; PRIOR APPLICATION NUMBER: US/09/964,824
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US/09/967,768
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: US/09/968,007
 ; PRIOR FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US/09/969,347
 ; PRIOR FILING DATE: 2001-10-02
 ; PRIOR APPLICATION NUMBER: US/09/969,708
 ; PRIOR FILING DATE: 2001-10-03
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 8447
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1447
 ; LENGTH: 2436
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-843-641A-1447

Alignment Scores: Length: 2436
 Pred. No.: 0.000187
 Score: 79.00 Matches: 15
 Percent Similarity: 93.75%
 Best Local Similarity: 93.75%
 Query Match: 95.18%
 Indels: 0
 Gaps: 0

US-10-030-937-72 (1-16) x US-10-843-641A-1447 (1-2436)

Qy 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
 Db 491 TACTCACTGCCCAAGAGCGAATTCGTTGTGCTGACCTGAGCTGCC 538

RESULT 8

US-10-170-385-390
 ; Sequence 390, Application US/10170385
 ; Publication No. US2003020372A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ward, Neil Raymond
 ; APPLICANT: Mundy, Christopher Robert

```
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingeman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268200100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-390

Alignment Scores:
Pred. No.: 0.00019 Length: 2478
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-72 (1-16) x US-10-170-385-390 (1-2478)

QY 1 TyrSerLeuProIysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 528 TACTCACTGCCCAAGAGCGAATTGGTTGCTGACCTGGAGCTGCC 575

RESULT 9
US-10-723-860-5187
; Sequence 5187, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5187
; LENGTH: 3988
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2864)..(2894)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3472)..(3486)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-5187

Alignment Scores:
Pred. No.: 0.000329 Length: 3988
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0

Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 20 Gaps: 0

US-10-030-937-72 (1-16) x US-10-723-860-5187 (1-3988)

QY 1 TyrSerLeuProIysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 528 TACTCACTGCCCAAGAGCGAATTGGTTGCTGACCTGGAGCTGCC 575

RESULT 10
US-10-225-810-26/c
; Sequence 26, Application US/10225810
; Publication No. US20030157512A1
; GENERAL INFORMATION:
; APPLICANT: Birmingham, Jr., John R.
; TITLE OF INVENTION: Tramdorins and Methods of Using Tramdorin
; FILE REFERENCE: McLaugh-07165
; CURRENT APPLICATION NUMBER: US/10/225,810
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 250000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (42953)..(43052)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (45557)..(45656)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (48203)..(48302)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (49551)..(49650)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51561)..(51660)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52722)..(52821)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (53864)..(53963)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (55290)..(55389)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (56674)..(56773)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (57879)..(57978)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (78952)..(79051)
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; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (85316)..(85415)
; OTHER INFORMATION: n is a, c, g, or t
US-10-225-810-26

Alignment Scores:
Pred. No.: 0.0379 Length: 250000
Score: 79.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 95.18% Indels: 0
DB: 16 Gaps: 0

US-10-030-937-72 (1-16) x US-10-225-810-26 (1-250000)

QY 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 249623 TACTCACTGCCAAGAGCGAATTCTGTTCCTGACTGGAGCTGCC 249576

RESULT 11

US-10-388-934-167
; Sequence 167, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
; APPLICANT: Boess, Franziska
; APPLICANT: Suter-Dick, Laura
; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; Sequence Filing Date: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-388-934-167

Alignment Scores:
Pred. No.: 0.0114 Length: 1983
Score: 69.00 Matches: 13
Percent Similarity: 81.25% Conservative: 0
Best Local Similarity: 81.25% Mismatches: 3
Query Match: 83.13% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-72 (1-16) x US-10-388-934-167 (1-1983)

QY 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 462 TACTCACTGCTTCGAGCAACTTCACAGTGCCTGATCTGGAGCTCCA 509

RESULT 12

US-10-972-079-7219
; Sequence 7219, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MM1110-2

; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7219
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Chicken 19866894191999_2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(32)
; OTHER INFORMATION: n is any nucleotide
US-10-972-079-7219

Alignment Scores:
Pred. No.: 0.00442 Length: 596
Score: 68.00 Matches: 12
Percent Similarity: 93.75% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 81.93% Indels: 0
DB: 22 Gaps: 0

US-10-030-937-72 (1-16) x US-10-972-079-7219 (1-596)

QY 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 353 TACTCACTGCCCGCCGAGCTTCGCTCCCTGCCGAGCTGCGGCC 400

RESULT 13

US-10-972-079-7218
; Sequence 7218, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7218
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Chicken 19866894191999_1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(114)
; OTHER INFORMATION: n is any nucleotide
US-10-972-079-7218

Alignment Scores:
Pred. No.: 0.00445 Length: 599
Score: 68.00 Matches: 12
Percent Similarity: 93.75% Conservative: 3
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 81.93% Indels: 0
DB: 22 Gaps: 0

US-10-030-937-72 (1-16) x US-10-972-079-7218 (1-599)

QY 1 TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 16
Db 435 TACTCACTGCCCGCCGAGCTTCGCTCCCTGCCGAGCTGCGGCC 482

RESULT 14

US-10-437-963-4335
; Sequence 4335, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 4335
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2269)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11228C.1
US-10-437-963-4335

Alignment Scores:

Pred. No.:	78.9	Length:	2269
Score:	49.00	Matches:	8
Percent Similarity:	92.31%	Conservative:	4
Best Local Similarity:	61.54%	Mismatches:	1
Query Match:	59.04%	Indels:	0
DB:	19	Gaps:	0

US-10-030-937-72 (1-16) x US-10-437-963-4335 (1-2269)

Qy 3 LeuProlySerGluPheAlaValProAspLeuGluLeu 15

Db 221 GTTCCACGAGTGAATTTCCATACCTGATTGGAGCTT 259

RESULT 15

US-10-021-323-4461/c
; Sequence 4461, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 4461
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3825-025-Q6-N6-C6
US-10-021-323-4461

Alignment Scores:

Pred. No.:	20.3	Length:	475
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Score:	48.00	Matches:	10
Percent Similarity:	73.33%	Conservative:	1
Best Local Similarity:	66.67%	Mismatches:	4
Query Match:	57.83%	Indels:	0
DB:	19	Gaps:	0

US-10-030-937-72 (1-16) x US-10-021-323-4461 (1-475)

Qy 2 SerLeuProlySerGluPheAlaValProAspLeuGluLeuPro 16

Db 435 TCCTTCCCCAGGGAACGATGTGTGCCCATTCCTGGAACTACCA 391

Search completed: July 27, 2005, 22:48:10

Job time : 106.631 secs

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OM protein - protein search, using sw model

Run on: July 27, 2005, 12:32:19 ; Search time 37.7422 Seconds
(without alignments)
381.728 Million cell updates/sec

Title: US-10-030-937-9
Perfect score: 1018
Sequence: 1 MQSLMQAPLLIALGILLATP.....LSSSGKRLGCIKIAASLKG1 193

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1005	98.7	193	4	US-09-183-841-1
2	857	84.2	178	4	US-09-183-841-2
3	88.5	8.7	310	4	US-09-976-594-807
4	86.5	8.5	410	3	US-08-630-172-17
5	86.5	8.5	410	3	US-09-375-419-17
6	86.5	8.5	768	3	US-09-302-812-8
7	86.5	8.5	768	3	US-09-511-477-8
8	86.5	8.5	768	3	US-09-511-507-8
9	86	8.4	143	4	US-09-860-793-3
10	83	8.2	572	6	5256770-7
11	83	8.2	572	6	5256770-7
12	82	8.1	446	1	US-08-307-444A-5
13	82	8.1	446	1	US-08-587-389-5
14	82	8.1	456	1	US-08-307-444A-3
15	82	8.1	456	1	US-08-307-444A-4
16	82	8.1	456	1	US-08-587-389-3
17	82	8.1	456	1	US-08-587-389-4
18	82	8.1	475	1	US-08-307-444A-1
19	82	8.1	475	1	US-08-307-444A-2
20	82	8.1	475	1	US-08-587-389-1
21	82	8.1	475	1	US-08-587-389-2
22	82	8.1	476	1	US-08-014-723-1
23	82	8.1	476	1	US-08-014-723-2
24	82	8.1	476	1	US-08-014-723-18
25	82	8.1	476	1	US-08-110-011A-1
26	82	8.1	476	1	US-08-110-011A-2
27	82	8.1	476	1	US-08-110-011A-18

28	82	8.1	494	1	US-08-014-723-14	Sequence 14, Appl
29	82	8.1	494	1	US-08-014-723-16	Sequence 16, Appl
30	82	8.1	494	1	US-08-110-011A-14	Sequence 14, Appl
31	82	8.1	494	1	US-08-110-011A-16	Sequence 16, Appl
32	82	8.1	497	1	US-08-312-870-3	Sequence 3, Appl
33	82	8.1	497	4	US-09-331-793-4	Sequence 3, Appl
34	82	8.1	498	2	US-08-733-564-2	Sequence 2, Appl
35	82	8.1	516	4	US-09-509-994-1	Sequence 1, Appl
36	82	8.1	516	4	US-09-509-994-2	Sequence 2, Appl
37	82	8.1	575	1	US-08-261-206A-59	Sequence 59, Appl
38	82	8.1	575	1	US-08-312-870-1	Sequence 1, Appl
39	82	8.1	575	1	US-08-170-290A-54	Sequence 54, Appl
40	82	8.1	575	4	US-09-880-484D-2	Sequence 2, Appl
41	82	8.1	575	4	US-10-438-648-2	Sequence 2, Appl
42	82	8.1	575	6	5466668-6	Patent No. 5466668
43	82	8.1	575	6	5466668-6	Patent No. 5466668
44	82	8.1	746	4	US-09-370-838-185	Sequence 185, App
45	82	8.1	746	4	US-09-854-133-185	Sequence 185, App

ALIGNMENTS

RESULT 1
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183.841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (33)..(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1

Query Match	98.7%	Score 1005;	DB 4;	Length 193;
Best Local Similarity	99.0%	Pred. No. 5.5e-110;	Mismatches 2;	Indels 0;
Matches 191;	Conservative 0;			Gaps 0;
Qy	1	MQSLMQAPLLIALGILLATPAAHLKKPSQLSSFSWNCDFEGKDPVIRSLTLEPDPVIV	60	
Db	1	MQSLMQAPLLIALGILLATPAAHLKKPSQLSSFSWNCDFEGKDPVIRSLTLEPDPVIV	60	
Qy	61	PGNVTLSVVGSTSVPLSPKVDLVLEKEVAGLMIKIPCTDIYIGSCTPEHFCVDLMDLIP	120	
Db	61	PGNVTLSVVGSTSVPLSPKVDLVLEKEVAGLMIKIPCTDIYIGSCTPEHFCVDLMDLIP	120	
Qy	121	TGBCPCPEPLRYGLPCHCPKFGYSLPKSEFAVPDLPSPMLTTGNVRIEVLSSSGKR	180	
Db	121	TGBCPCPEPLRYGLPCHCPKFGYSLPKSEFAVPDLPSPMLTTGNVRIEVLSSSGKR	180	
Qy	181	LGCIKIAASLKG1	193	
Db	181	LGCIKIAASLKG1	193	

RESULT 2
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:

APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: van20010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match 84.2%; Score 857; DB 4; Length 178;
Best Local Similarity 98.8%; Pred. No. 1.3e-92;
Matches 160; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 32 SSFSDNCFEGKDPKPAVIRSLTLEPDPPIVPGNVTLSVVGSTSVPLSSPLKVDLVLEKEVA 91
DB 17 SSFSDNCFEGKDPKPAVIRSLTLEPDPPIVPGNVTLSVVGSTSVPLSSPLKVDLVLEKEVA 76

QY 92 GLWIKIPCTDIYIGSCTFEHCDFCDVLDMLIPTGBCPCPEPLRTYGLPCHCPKFGTYSLPKSE 151
DB 77 GLWIKIPCTDIYIGSCTFEHCDFCDVLDMLIPTGBCPCPEPLRTYGLPCHCPKFGTYSLPKSE 136

QY 152 FAVPDLLELPSWLTGNYRIESVLSSGKRLGCIKIAASLKGI 193
DB 137 FVVPDLLELPSWLTGNYRIESVLSSGKRLGCIKIAASLKGI 178

RESULT 3
US-09-976-594-807
; Sequence 807, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 807
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2770104CD1
US-09-976-594-807

Query Match 8.7%; Score 88.5; DB 4; Length 310;
Best Local Similarity 24.7%; Pred. No. 0.081;
Matches 55; Conservative 20; Mismatches 67; Indels 81; Gaps 10;

QY 9 LLIALGILLATPAQAH---LKKPSQLSSFSWDCNCFEGKDPKPAVIRSLTLEPDPPIVPGN-V 64
DB 51 VLLICGLSLGPRTHVQTGTIPKP-----TWABPDSVITQGSVP 89

QY 65 TLSVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTD-----YIGSCTFEH----- 110
DB 90 TLSQQSLEAQ-----EYRLYREKKS-WITRIRPELVNGQFHLPSITWEHTGYGCO 143

QY 111 -----FCVDVLDMLI-----PTGBCPCPEPLRTYV-----LPCHCPKFGTYSLPKSE 151

DB 144 YYSRARWSELSDPLVAGDDRSYQNFTSQSPGPGVVTPGKNVTLQCQSRGQHFHTLLTKEG 203

QY 152 FAVPDLLELPS-----WLTTCNVRIESVLSS 177
DB 204 AGHPPLHLRSEHQAOQNAEPRMGPVTSAHVGYRCYSSLSN 246

RESULT 4
US-08-630-172-17
; Sequence 17, Application US/08630172
; Patent No. 6060054
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,172
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-630-172-17

Query Match 8.5%; Score 86.5; DB 3; Length 410;
Best Local Similarity 25.6%; Pred. No. 0.21;
Matches 42; Conservative 14; Mismatches 43; Indels 65; Gaps 9;

QY 26 KKPSQLSSFS-----WDCNCFEGKDPKPAVIRSLTLEPDPPIV-----PGNVTLSVVGST- 72
DB 46 KGPSKLNDRADSRRLWD---QCNFLIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA 102

QY 73 -----SVPLSSP-----LKVDLVLEKEVAGLWIKIP 98
DB 103 NSDTHLLQGSLLTLTLESPPGSSPVQCKSPRGKNIQGGKTLVS-QLELQDAGTWI--- 158

QY 99 CTDTYIGSCTFEHCDFCDVLDMLIPTG---BPCPEPLRTYGLPCHCP 139
DB 159 CTVLQNKQKVEFKIDIVVLAEPGRGTIKPCP-----PCKCP 194

RESULT 5
US-09-375-419-17
; Sequence 17, Application US/09375419
; Patent No. 6264950
; GENERAL INFORMATION:
; APPLICANT: Staerz, Uwe
; TITLE OF INVENTION: NOVEL PRODUCT AND PROCESS FOR T
; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, 35th Floor
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/375,419
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,172
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-375-419-17

Query Match 8.5%; Score 86.5; DB 3; Length 410;
Best Local Similarity 25.6%; Pred. No. 0.21;
Matches 42; Conservative 14; Mismatches 43; Indels 65; Gaps 9;

QY 26 KKPQLSSPFS-----WDNCFEGKDPVIRSLTLEPDPPIV-----PGNVTLSVVGST- 72
DB 46 KGPSKLNDRADSRSLWD---QGNPFLIIKNLKIEDSDTVICBVEQKEVQLLVFLTA 102
QY 73 -----SVPLSSP-----LKVDLVLEKEVAGLWIKIP 98
DB 103 NSDTHLQGSQSLTLESPGSSPVCQRSPGKNIQGGKTLSSV-QLELQDAGTWI--- 158
QY 99 CTDYIGSCTFEHFCVDVLDMLIPTG---EPCPEPLRTYGLPCHCP 139
DB 159 CTVLQNKQKVEFKIDIVLAEPKRGPTIKPCP-----PCKCP 194

RESULT 6
US-09-302-812-8
; Sequence 8, Application US/093028128
; Patent No. 6333148
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/302,812B
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,768
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 768
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

; FEATURE:
US-09-302-812-8

Query Match 8.5%; Score 86.5; DB 3; Length 768;
Best Local Similarity 25.4%; Pred. No. 0.52;
Matches 53; Conservative 25; Mismatches 94; Indels 37; Gaps 9;

QY 3 SLMQAPLLIALGLLATPAQAHLLKPKSQLSSP---SWDNCPEGKDPVIRSL----- 51
DB 245 SOQIISCLLANAFLCTFPRRNTLKRKSEYSTPDDINFNRLYQSTGPAVLEKLCIMHYPR 304
QY 52 ---TLEPDPPIVVGNNVTLSSVGS-----TSVPLSS-PLKVLDL--VLEKEVAGLW 94
DB 305 RVCPTERDASNVPTGVVTFVRRESGLPEHLIDWSQSAAPLGVDVPLHVDAGTIEDGIGLL 364
QY 95 IKIPCTDYIGSCTFEHFC--DVLDMLIPTGECPEPL-RTYGLPCHCPKEGTYSLPKSE 151
DB 365 QVDFANKYLGGLGVGHGCVQEBIRFVI-----CPELLVGLKFTCLRPPEALVMLGAER 418
QY 152 FAVPDLPLPSWLTTCNRYIESVLSSSGKR 180
DB 419 YSNYTYAGSFEWSGNFEDSTPRDSSGRR 447

RESULT 7

US-09-511-477-8
; Sequence 8, Application US/09511477
; Patent No. 6337202
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AME, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZ
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/511,477
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 09/302,812
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 768
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
US-09-511-477-8

Query Match 8.5%; Score 86.5; DB 3; Length 768;
Best Local Similarity 25.4%; Pred. No. 0.52;
Matches 53; Conservative 25; Mismatches 94; Indels 37; Gaps 9;

QY 3 SLMQAPLLIALGLLATPAQAHLLKPKSQLSSP---SWDNCPEGKDPVIRSL----- 51
DB 245 SOQIISCLLANAFLCTFPRRNTLKRKSEYSTPDDINFNRLYQSTGPAVLEKLCIMHYPR 304
QY 52 ---TLEPDPPIVVGNNVTLSSVGS-----TSVPLSS-PLKVLDL--VLEKEVAGLW 94
DB 305 RVCPTERDASNVPTGVVTFVRRESGLPEHLIDWSQSAAPLGVDVPLHVDAGTIEDGIGLL 364
QY 95 IKIPCTDYIGSCTFEHFC--DVLDMLIPTGECPEPL-RTYGLPCHCPKEGTYSLPKSE 151
DB 365 QVDFANKYLGGLGVGHGCVQEBIRFVI-----CPELLVGLKFTCLRPPEALVMLGAER 418
QY 152 FAVPDLPLPSWLTTCNRYIESVLSSSGKR 180
DB 419 YSNYTYAGSFEWSGNFEDSTPRDSSGRR 447

RESULT 8

US-09-511-507-8
; Sequence 8, Application US/09511507

Db 186 AAVSITGTTPFAARGADFOALPVGSSAA--VAPLGQLMCTAGNVQGHWAREAPGAW--- 240
QY 98 PCTDIYIGSCFHFCDVLDMLIPTGBCPEP-----LRTYGLPCHCPKPGKGTYSLPKSEFA 153
Db 241 DCSVENGGC--EHACNA-----IFGAPRCQCPAGAALOADGRSCTASATQSCNDLCB-HFC 293
QY 154 VPDLPLPSWLTGNYRIESVLSSSGKRL 181
Db 294 VNPDPQ-----GSY---SCMCETGYRL 313

RESULT 12

US-08-307-444A-5
; Sequence 5, Application US/08307444A
; Patent No. 5516659
; GENERAL INFORMATION:
; APPLICANT: NII, ATSUSHI
; APPLICANT: MORISHITA, HIDEAKI
; APPLICANT: UEMURA, AKIO
; APPLICANT: MOCHIDA, EI
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,444A
; FILING DATE: 19-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,436
; FILING DATE: 26-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: OLIFF, JAMES A.
; REGISTRATION NUMBER: 27,075
; REFERENCE/DOCKET NUMBER: JAO 27706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; TELEX: 90-1799 PTO ALEX
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-307-444A-5

Query Match 8.1%; Score 82; DB 1; Length 446;
Best Local Similarity 23.3%; Pred. No. 0.8;
Matches 49; Conservative 23; Mismatches 74; Indels 64; Gaps 12;

QY 8 PLLIALGLLLAT-----PAQAHLKPSQLSSFSWDCNCFEGKDPAVIRSLTLEPDPV 59
Db 117 PLCVAVSAEATVPSEPIWEEQCEVKADGFLCEFH-----PATCRPLAVEFGAAA 168
QY 60 VPGNVTLSV-----VGSTSVPLSSPLKVDLVL-----EKEVAGLWI 95
Db 169 AAVSITGTTPFAARGADFOALPVGSSAA--VAPLGQLMCTAPPGAVQGHWAREAPGAW- 225

QY 96 KIPCTDIYIGSCFHFCDVLDMLIPTGBCPEP-----LRTYGLPCHCPKPGKGTYSLPKSE 151
Db 226 --DCSVENGGC--EHACNA-----IFGAPRCQCPAGAALOADGRSCTASATQSCNDLCB-H 276
QY 152 FAVPDLPLPSWLTGNYRIESVLSSSGKRL 181
Db 277 FCVPNPDP-----GSY---SCMCETGYRL 298

RESULT 13

US-08-587-389-5
; Sequence 5, Application US/08587389
; Patent No. 565964
; GENERAL INFORMATION:
; APPLICANT: NII, ATSUSHI
; APPLICANT: MORISHITA, HIDEAKI
; APPLICANT: UEMURA, AKIO
; APPLICANT: MOCHIDA, EI
; TITLE OF INVENTION: TRUNCATED THROMBOMODULIN, RECOMBINANT
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,389
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,444
; FILING DATE: 19-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OLIFF, JAMES A.
; REGISTRATION NUMBER: 27,075
; REFERENCE/DOCKET NUMBER: JAO 27706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; TELEX: 90-1799 PTO ALEX
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-587-389-5

Query Match 8.1%; Score 82; DB 1; Length 446;
Best Local Similarity 23.3%; Pred. No. 0.8;
Matches 49; Conservative 23; Mismatches 74; Indels 64; Gaps 12;

QY 8 PLLIALGLLLAT-----PAQAHLKPSQLSSFSWDCNCFEGKDPAVIRSLTLEPDPV 59
Db 117 PLCVAVSAEATVPSEPIWEEQCEVKADGFLCEFH-----PATCRPLAVEFGAAA 168
QY 60 VPGNVTLSV-----VGSTSVPLSSPLKVDLVL-----EKEVAGLWI 95
Db 169 AAVSITGTTPFAARGADFOALPVGSSAA--VAPLGQLMCTAPPGAVQGHWAREAPGAW- 225
QY 96 KIPCTDIYIGSCFHFCDVLDMLIPTGBCPEP-----LRTYGLPCHCPKPGKGTYSLPKSE 151

```

Db      226  --DCSVENGCC--EHACNA-----IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCE-H 276
Qy      152 FAVPDLELPWLTTGNRYIESVLSGKRL 181
Db      277 FCVPNDQP-----GSY---SCMCETGYRL 298

RESULT 14
US-08-307-444A-3
; Sequence 3, Application US/08307444A
; Patent No. 5516659
; GENERAL INFORMATION:
; APPLICANT: NII, ATSUSHI
; APPLICANT: MORISHITA, HIDEAKI
; APPLICANT: UEMURA, AKIO
; APPLICANT: MOCHIDA, EI
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,444A
; FILING DATE: 19-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,436
; FILING DATE: 26-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: OLIFF, JAMES A.
; REGISTRATION NUMBER: 27,075
; REFERENCE/DOCKET NUMBER: JAO 27706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; TELEX: 90-1799 PTO ALEX
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 456 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-307-444A-3

Query Match      8.1%; Score 82; DB 1; Length 456;
Best Local Similarity 23.3%; Pred. No. 0.83;
Matches 49; Conservative 23; Mismatches 74; Indels 64; Gaps 12;

Qy      8 PLLIALGLLLAT-----PAQAHKKPSQLSSFSMDNCFCGKDPVAVIRSLTLEPDPV 59
Db      117 PLCVAVSAEATVPSEPIWEQCEVKADGFLCEFH-----PATCRPLAVEPGAA 168
Qy      60 VPGNVTLVS-----VGSTSVPLSSPLKVDLVL-----EKEVAGLWI 95
Db      169 AAVSITYGTPFAARGADFOALPVGSSAA--VAPLGLQLMCTAPPVAGVGHWAREAPGAW- 225
Qy      96 KIPCTDYIGSCTFEHFCVDLMDLIPTGCPPEP-----LRTVGLPCHCPFKEGTYSLPKSE 151
Db      226  --DCSVENGCC--EHACNA-----IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCE-H 276
Qy      152 FAVPDLELPWLTTGNRYIESVLSGKRL 181
Db      277 FCVPNDQP-----GSY---SCMCETGYRL 298

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Db      277 FCVPNDQP-----GSY---SCMCETGYRL 298

RESULT 15
US-08-307-444A-4
; Sequence 4, Application US/08307444A
; Patent No. 5516659
; GENERAL INFORMATION:
; APPLICANT: NII, ATSUSHI
; APPLICANT: MORISHITA, HIDEAKI
; APPLICANT: UEMURA, AKIO
; APPLICANT: MOCHIDA, EI
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,444A
; FILING DATE: 19-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,436
; FILING DATE: 26-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: OLIFF, JAMES A.
; REGISTRATION NUMBER: 27,075
; REFERENCE/DOCKET NUMBER: JAO 27706
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; TELEX: 90-1799 PTO ALEX
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 456 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-307-444A-4

Query Match      8.1%; Score 82; DB 1; Length 456;
Best Local Similarity 23.3%; Pred. No. 0.83;
Matches 49; Conservative 23; Mismatches 74; Indels 64; Gaps 12;

Qy      8 PLLIALGLLLAT-----PAQAHKKPSQLSSFSMDNCFCGKDPVAVIRSLTLEPDPV 59
Db      117 PLCVAVSAEATVPSEPIWEQCEVKADGFLCEFH-----PATCRPLAVEPGAA 168
Qy      60 VPGNVTLVS-----VGSTSVPLSSPLKVDLVL-----EKEVAGLWI 95
Db      169 AAVSITYGTPFAARGADFOALPVGSSAA--VAPLGLQLMCTAPPVAGVGHWAREAPGAW- 225
Qy      96 KIPCTDYIGSCTFEHFCVDLMDLIPTGCPPEP-----LRTVGLPCHCPFKEGTYSLPKSE 151
Db      226  --DCSVENGCC--EHACNA-----IPGAPRCQCPAGAAQADGRSCTASATQSCNDLCE-H 276
Qy      152 FAVPDLELPWLTTGNRYIESVLSGKRL 181
Db      277 FCVPNDQP-----GSY---SCMCETGYRL 298

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Search completed: July 27, 2005, 18:59:18
Job time : 38.7422 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 18:09:01 ; Search time 422.884 Seconds
(without alignments)
177.532 Million cell updates/sec

Title: US-10-030-937-9

Perfect score: 1018

Sequence: 1 MQSLMQAPLLIALGILLATP.....LSSSGRRGLGCIKAASLKGI 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1005	98.7	193	15 US-10-170-385-389	Sequence 389, App
2	1000	98.2	193	16 US-10-723-860-529	Sequence 529, App
3	412	40.5	191	15 US-10-264-049-2611	Sequence 2611, Ap
4	353	34.7	61	9 US-09-854-761-34809	Sequence 34809, A
5	162.5	16.0	126	10 US-09-764-891-4977	Sequence 4977, Ap
6	98.5	9.7	273	16 US-10-425-115-297138	Sequence 297138,
7	91.5	9.0	641	15 US-10-369-493-20746	Sequence 20746, A
8	90	8.8	651	15 US-10-369-493-20109	Sequence 20109, A
9	88	8.5	796	16 US-10-437-963-187458	Sequence 187458,
10	86.5	8.5	196	16 US-10-425-115-251307	Sequence 251307,
11	86.5	8.5	574	16 US-10-725-013-2	Sequence 2, Appli

12	86.5	8.5	768	9 US-09-973-451-8	Sequence 8, Appli
13	86	8.4	143	9 US-09-860-793-3	Sequence 3, Appli
14	86	8.4	474	15 US-10-369-493-19074	Sequence 19074, A
15	86	8.4	575	15 US-10-094-886-196	Sequence 196, App
16	86	8.4	611	15 US-10-369-493-7417	Sequence 7417, Ap
17	86	8.4	633	15 US-10-369-493-4658	Sequence 4658, Ap
18	86	8.4	2293	16 US-10-032-438B-2	Sequence 2, Appli
19	84	8.3	490	16 US-10-437-963-180789	Sequence 180789,
20	83.5	8.2	132	15 US-10-424-599-255741	Sequence 255741,
21	83	8.2	688	15 US-10-282-122A-47772	Sequence 47772, A
22	82.5	8.1	342	16 US-10-425-115-220322	Sequence 220322,
23	82.5	8.1	342	16 US-10-425-115-220323	Sequence 220323,
24	82.5	8.1	352	15 US-10-425-114-63175	Sequence 63175, A
25	82.5	8.1	371	15 US-10-425-114-62424	Sequence 62424, A
26	82.5	8.1	372	15 US-10-425-114-53454	Sequence 53454, A
27	82.5	8.1	372	15 US-10-425-114-72059	Sequence 72059, A
28	82.5	8.1	375	15 US-10-425-114-58493	Sequence 58493, A
29	82.5	8.1	792	14 US-10-309-422-38	Sequence 38, Appli
30	82.5	8.1	824	16 US-10-467-595-4	Sequence 4, Appli
31	82.5	8.1	926	14 US-10-309-422-36	Sequence 36, Appli
32	82.5	8.1	957	14 US-10-309-422-14	Sequence 14, Appli
33	82.5	8.1	958	14 US-10-309-422-26	Sequence 26, Appli
34	82.5	8.1	1091	14 US-10-309-422-12	Sequence 12, Appli
35	82.5	8.1	1092	14 US-10-309-422-24	Sequence 24, Appli
36	82	8.1	497	15 US-10-298-796-4	Sequence 4, Appli
37	82	8.1	575	9 US-09-938-405-2	Sequence 3, Appli
38	82	8.1	575	14 US-10-150-440-3	Sequence 2, Appli
39	82	8.1	575	14 US-10-438-648-2	Sequence 2, Appli
40	82	8.1	575	15 US-10-410-195-2	Sequence 2, Appli
41	82	8.1	575	15 US-10-373-801-29	Sequence 29, Appli
42	82	8.1	575	17 US-10-785-156-2	Sequence 2, Appli
43	82	8.1	575	18 US-10-712-124-110	Sequence 110, App
44	82	8.1	631	14 US-10-150-440-1	Sequence 1, Appli
45	82	8.1	631	16 US-10-741-601-309	Sequence 309, App

ALIGNMENTS

RESULT 1

US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

Query Match 98.7%; Score 1005; DB 15; Length 193;
Best Local Similarity 99.0%; Pred. No. 8.8e-97;
Matches 191; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 MQSLMQAPLLIALGILLATPAQAHLKKPSQLSSFSWDCNCEGKDPVIRSLTLEPDPV 60
Db 1 MQSLMQAPLLIALGILLATPAQAHLKKPSQLSSFSWDCNCEGKDPVIRSLTLEPDPV 60
Qy 61 PGNVTLVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDYIGSCTFEHFCVDVLDMLIP 120
Db 61 PGNVTLVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDYIGSCTFEHFCVDVLDMLIP 120
Qy 121 TGEPCPEPLRTYGLPCHCPKPEGYSPLPKSEFAVPDLELPSWLTGNYRIESVLSGSKR 180
Db 121 TGEPCPEPLRTYGLPCHCPKPEGYSPLPKSEFAVPDLELPSWLTGNYRIESVLSGSKR 180
Qy 181 LGCICKIAASLXGI 193
Db 181 LGCICKIAASLXGI 193

RESULT 2
US-10-723-860-529
; Sequence 529, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 03882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 529
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-529

Query Match 98.2%; Score 1000; DB 16; Length 193;
Best Local Similarity 98.4%; Pred. No. 2.9e-96;
Matches 190; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MQSLMQAPLLIALGILLATPAQAHLKKPSQLSSFSWDCNCEGKDPVIRSLTLEPDPV 60
Db 1 MQSLMQAPLLIALGILLATPAQAHLKKPSQLSSFSWDCNCEGKDPVIRSLTLEPDPV 60
Qy 61 PGNVTLVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDYIGSCTFEHFCVDVLDMLIP 120
Db 61 PGNVTLVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDYIGSCTFEHFCVDVLDMLIP 120
Qy 121 TGEPCPEPLRTYGLPCHCPKPEGYSPLPKSEFAVPDLELPSWLTGNYRIESVLSGSKR 180
Db 121 TGEPCPEPLRTYGLPCHCPKPEGYSPLPKSEFAVPDLELPSWLTGNYRIESVLSGSKR 180
Qy 181 LGCICKIAASLXGI 193
Db 181 LGCICKIAASLXGI 193

RESULT 3
US-10-264-049-2611
; Sequence 2611, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
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; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patent in Ver. 3.1
; SEQ ID NO 2611
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (141)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (142)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (184)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (187)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-2611

Query Match 40.5%; Score 412; DB 15; Length 191;
Best Local Similarity 48.4%; Pred. No. 1.2e-34;
Matches 78; Conservative 24; Mismatches 51; Indels 8; Gaps 2;

Qy 13 LGLLA-----TPQAHLKKPSQLSSFSWDCNCEGKDPVIRSLTLEPDPVPGNV 65
Db 24 LGLLAGPAHAHVPAHPVNPPOVISFFWENCHERKDPVLKSMTLEPDPPIAYPGNV 83
Qy 66 LSVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDYIGSCTFEHFCVDVLDMLIPTGEP 125
Db 84 ISAEQLVRVPLSPQKVELIIEKKVANFWIKVPCMSHV-RCIFEDICQILDFLIPPQXX 142
Qy 126 PEPLRTYGLPCHCPKPEGYSPLPKSEFAVPDLELPSWLTG 166
Db 143 PEPLRTYGLPCTVPSSRHLLNAQRLKPCPNTDLPGLITSG 183

RESULT 4
US-09-864-761-34809
; Sequence 34809, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34809
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011342.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EST HUMAN HIT: BE182886.1, EVALUATE 9.00e-34
; OTHER INFORMATION: SWISSPROT HIT: P17900, EVALUATE 1.00e-34
US-09-864-761-34809

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Query Match 34.7%; Score 353; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.9e-29;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 82 VDLVLEKEVAGLWIKIPCTDYIGCTFEHFCVDLMDLIPTGECPEPLRTYGLPCHCPK 141
DB 1 VDLVLEKEVAGLWIKIPCTDYIGCTFEHFCVDLMDLIPTGECPEPLRTYGLPCHCPK 60

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QY 142 E 142
DB 61 E 61

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RESULT 5
US-09-764-891-4977
; Sequence 4977, Application US/05764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4977
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (119)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-4977

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Query Match 16.0%; Score 162.5; DB 10; Length 126;
Best Local Similarity 54.2%; Pred. No. 9.2e-09;
Matches 32; Conservative 7; Mismatches 13; Indels 7; Gaps 1;
QY 13 LGLLLA-----TPQAHLKKPSQLSSFSWDCNCFEGKDPVIRSLTLPDPTVWPGNV 64
DB 24 LGLLLAGPAHAHVPAHAPVNPFPQVISFWENCHERKDPVLLKSWTLSEPDPIAYPGNV 82

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RESULT 6

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US-10-425-115-297138
; Sequence 297138, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 297138
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_34069C.1.pap
US-10-425-115-297138

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Query Match 9.7%; Score 98.5; DB 16; Length 273;
Best Local Similarity 26.7%; Pred. No. 0.13;
Matches 59; Conservative 24; Mismatches 73; Indels 65; Gaps 14;

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QY 3 SLMOAPL---LIALGLLLATPAQHLKK-----PSQLSSFSWDCNCFEGKDPVIRSLTLPDPTVWPGNV 50
DB 70 ALLPALPASLPFAASILYSLQAVLPKCGISLCPAELAPA--PSCSSRRPPAPLAWSS 127
QY 51 LTLEPDPVIVPGNVTLVVGTSVPLSSPLKV-----DLVLEKEVAGLW----- 94
DB 128 SFLVPVPCVFP--VTSMAPSL--PLUSSPLRVPLVSSLRARSFLCVPAATSLWCLPFA 184
QY 95 -IKIPCTDYIGCTFEHFCVDLMDLIPTGECPEPLRTYGLPCH-----CPPKEGTY 145
DB 185 RAKFPCLSLALGPC-----STVPCFSARV-KFPCRVCLGRKPCVCPRR--AC 227
QY 146 SLPKSEFAVDPDLPSWLTGNYRIESVLSSSG--KRLGCI 184
DB 228 CSPKR----PMLQRPVFSMSFHVGIVSVVSSSGINKQTGAV 264

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RESULT 7

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US-10-369-493-20746
; Sequence 20746, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

```

APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20746
LENGTH: 641
TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
US-10-369-493-20746

Query Match 9.0%; Score 91.5; DB 15; Length 641;
Best Local Similarity 25.4%; Pred. No. 2.2;
Matches 47; Conservative 30; Mismatches 63; Indels 45; Gaps 11;
Qy 45 PAVIRSLTLEPD-PIVVPGNVTLVSGSTVPLS-----SPLKVDLVLEK 88
Db 351 PTAIRALMQADEPVKTKSRKSLGLSVGEPINPEAWYHRVVGEDRCPI-VDTWQOT 409
Qy 89 EVAGLWI-KIPCTDYI--GSCTFEHFCVDVLDMLIP-----TGBPC-----PEPLRT 131
Db 410 ETGGILITPLPGATKLKXGSAIRPFVGVVPEILDPEGNVLEGECTGNLCLARSWPGQWRT 469
Qy 132 -YGLPCHCPFKEGTYSLPKSEFV-----PDLEPLSWLTTGNYRIESVLSGSKRLGCIG 185
Db 470 VYG--DHARFQTVFESAYKGYFTGDGCRDITDGFYITG---RVDDVINVSGHRMGTA 524
Qy 186 IAAASL 190
Db 525 VESSL 529

RESULT 8
US-10-369-493-20109
Sequence 20109, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20109
LENGTH: 651
TYPE: PRT
ORGANISM: No. US20030233675A1toc punctiforme
US-10-369-493-20109

Query Match 8.8%; Score 90; DB 15; Length 651;
Best Local Similarity 27.2%; Pred. No. 3.2;
Matches 41; Conservative 22; Mismatches 50; Indels 38; Gaps 9;
Qy 68 VVGSTVPSLSPKVDLVLEKEVAGLWI-----KIPCTDYIGSCTFEH---FCDVLDW-- 117
Db 404 VIGDRCP-----VDTWQVETGIMITPLPGAIPKPG--GSATLPPGIADVDVLE 456
Qy 118 -LIPG-----PCPEPLRT-YGLP-----CHCPKEGTYSLPKSEFVDPLEL 159
Db 457 NTVPNNEGGYLAVRHPWPGMMRTVYGDPERFRTYWEHIPQDQGYTFYAGDGAQDB 516

Qy 160 PSWLTGNYRIESVLSGSKRLGCIGKIAASL 190
Db 517 YFWVMG---RVDDVLNVSGHRLGTMEVESAL 544
RESULT 9
US-10-437-963-187458
Sequence 187458, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 187458
LENGTH: 796
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_84159C.1.pap
US-10-437-963-187458

Query Match 8.6%; Score 88; DB 16; Length 796;
Best Local Similarity 24.2%; Pred. No. 6.7; Indels 94; Gaps 12;
Matches 57; Conservative 22; Mismatches 63; Indels 94; Gaps 12;
Qy 24 HLKKPSQLSSFSWDCNCFEGKDPVIRSLTLEPPPIV-----VPGNVTL----- 66
Db 108 NLKAS-----DNEFTGKLPDVLGSLTELDVLNCRISENLETWDFSKPAALTMLF 160
Qy 67 ----SVVGSTVPSLSPKV-DLVLEKEVAG-----PEHFCVDVLD-MLIPTGECPCPEPLRTYGLPCH 137
Db 161 LGNNSLIGTLPDVVISLKVYNNLVANNIVLGSTKNSDISTGSDNTIYEADATNLGDASY 220
Qy 93 ----LWIKIPCTDYIGSCT-----PEHFCVDVLD-MLIPTGECPCPEPLRTYGLPCH 137
Db 221 YVTDQIRW-GVSNVGVFYQATDRMDIYYSSEHFQTAVDKLFETARMSPSLSRYGL--- 276
Qy 138 CPPKEGTYS--LPKSEFVDPLEPLSWLTTGNYRIESVLSGSKRLGCIGKIAASLK 191
Db 277 -GLENGNYTVMLOFAEFAPDTQ--TWL-----SLGRRIFDIYVQGALK 317

RESULT 10
US-10-425-115-251307
Sequence 251307, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 251307
LENGTH: 196
TYPE: PRT
ORGANISM: Zea mays
FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_160777C.1.pap
US-10-425-115-251307

Query Match 8.5%; Score 86.5; DB 16; Length 196;
Best Local Similarity 19.1%; Pred. No. 1.5;
Matches 41; Conservative 37; Mismatches 74; Indels 63; Gaps 8;

QY 4 LMQAPLIAL--GILLATPA-----QAHK-----KPSQLS 32
DB 1 MLSTLLALLTSTLALASPVLPRGLQANAEVVLNGVSWGANKLSHVGTDDAGQVGTLT 60
QY 33 SPWDNCFEGKDPAVIRSLTLEDPDPIVPGNVTLSVVGTSVPLSVPLKVDLVLEKEVAG 92
DB 61 KDWTCGSPSDALQDSIKISDPKPGQDLIVASGRAQSKIDGTGVADVTVKGLK 120
QY 93 LWIKIPCTDYIGSCTFEHFCVDLMDLIPGECPEPLRTYGLPCHCPKEGTYSLPKSEF 152
DB 121 LLTK-----TFD-VCDELNANAT-----LRCPAPGTHSITQT-- 153
QY 153 AVPDLELPWLTGNVRIES-VLSSSGKRLGCIKI 186
DB 154 ----VALPREIPRAKFQVDALVYTODEEPAACINL 184

RESULT 11
US-10-725-013-2
; Sequence 2, Application US/10725013
; Publication No. US20040198683A1
; GENERAL INFORMATION:
; APPLICANT: Sehgal, Lakshman R.
; APPLICANT: Wong, Jonathan
; TITLE OF INVENTION: Ex vivo and in vivo expression of the thrombomodulin gene
; TITLE OF INVENTION: for the treatment of cardiovascular and peripheral vascular disease
; FILE REFERENCE: 3840-005-27
; CURRENT APPLICATION NUMBER: US/10/725,013
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/430,099
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-725-013-2

Query Match 8.5%; Score 86.5; DB 16; Length 574;
Best Local Similarity 24.1%; Pred. No. 6.3;
Matches 51; Conservative 27; Mismatches 71; Indels 69; Gaps 13;

QY 8 PLLIALGLLLAT-----PAQHLKPKPSQLSFSWDCNCFEGKDPVIRSLTLEDPDPIV 59
DB 135 PLCVAVSAEATVPSPINEEQCEVKADGFLCEHF-----PATCRPLAVEPGAA 186
QY 60 VPGNVTLSV-----VGSTSVPLSVPLKVDLV-----EKEVAGLWI 95
DB 187 AAVSYITGTPFAARGADFOALPVGSSAA--VAPLGLQLMCTAPPAGVQGWAREAPGAW- 243
QY 96 KIPCTDYIGSCTFEHFCVDLMDLIPGECPEP-----LRTYGLPCHCPKEGTYSLPK-- 149
DB 244 --DCSVENGCC--EHACNA-----IPGAPCQCAGAAQADGRSC-----TASTQSCNDLC 291
QY 150 SEFAPVDPLEPWSLTTGNVRIESVLSSSGKRL 181
DB 292 EHECFVNPDP-----GSY---SCMCTGYRL 315

RESULT 12
US-09-973-451-8
; Sequence 8, Application US/09973451
; Patent No. US20020132328A1
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.

; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE
; TITLE OF INVENTION: (PARG) ENZYMES,
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/973,451
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/302,812
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,768
; PRIOR FILING DATE: 1998-03-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 768
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
US-09-973-451-8

Query Match 8.5%; Score 86.5; DB 9; Length 768;
Best Local Similarity 25.4%; Pred. No. 9.2;
Matches 53; Conservative 25; Mismatches 94; Indels 37; Gaps 9;

QY 3 SLMQAPLIALGLLLATPAQHLKPKPSQLSSF---SWDCNCFEGKDPVIRSL----- 51
DB 245 SOQIISCLLANAFLCTFFRRNTLKRKSEYSTFPDINFNRLYQSTGTPAVLEKLCIMHYFR 304
QY 52 ---TLEPPDPIVPGNVTLSVVGSS-----TSVPLSS-PLKVDL--VLEKEVAGLW 94
DB 305 RYCPTERDASNVPTGVTVFRRSGLPEHLIDWSQAAPLGDVPLHVDAEGTIEDEIGILL 364
QY 95 IKIPCTDYIGSCTFEHFC--DVLDMLIPGECPEPL-RTYGLPCHCPKEGTYSLPKSE 151
DB 365 QVDFANKYLGGLVGHGCVQBEIRFVI-----CPLELVGKLFTECLURPF-EALVMLGAER 418
QY 152 FAVPDLELPWSLTTGNVRIESVLSSSGKR 180
DB 419 YSNYTGAGSPFWSGCFEDSITPRDSSGRR 447

RESULT 13
US-09-860-793-3
; Sequence 3, Application US/09860793
; Patent No. US20020136734A1
; GENERAL INFORMATION:
; APPLICANT: Pruett, John H
; APPLICANT: Temeyer, Kevin B
; APPLICANT: Kunz, Sidney E
; APPLICANT: Fisher, William F
; TITLE OF INVENTION: Vaccines for the Protection of Cattle from Psoroptic
; TITLE OF INVENTION: Scabies
; FILE REFERENCE: Docket 0047.96 - John H. Pruett et al.
; CURRENT APPLICATION NUMBER: US/09/860,793
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/366,603
; PRIOR FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 3
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Psoroptes ovis
US-09-860-793-3

Query Match 8.4%; Score 86; DB 9; Length 143;
Best Local Similarity 22.8%; Pred. No. 1.1;
Matches 43; Conservative 32; Mismatches 56; Indels 58; Gaps 10;
QY 10 LIALGLLLATPAQHLKPKPSQLSFSWDCNCFEGKDPVIRSLTLE---PDPITVPGNVTL 66

Db 5 LVLAITLAVVSAKVK-----FQDCGKE-----VESLEVEGSGDYCVIHKKKL 51

Qy 67 SV-VGSTVPLSPKVDLVEKEVAGLWIKIPCTDYIGSCTFEHFCVDLMDLPTGEP 125

Db 52 DLAISVTSNODSANLKLIV--ADINGVQIEVGVHDG-----88

Qy 126 PEPLRTYGLPCH---CPFKGTYSLPKSEFAPVDPLELPSWLTGTVNRIEVSLSGKRLG 182

Db 89 -----CHYVKCPKGGQHPDVKYVYSIPAI-LP---TTKAKIIAKIIGDKGLG-G 133

Qy 183 CIKIASLK 191

Db 134 CIVINGEQ 142

RESULT 14

US-10-369-493-19074

Sequence 19074, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 19074

LENGTH: 474

TYPE: PRT

ORGANISM: Anabaena PCC7120

US-10-369-493-19074

Query Match 8.4%; Score 86; DB 15; Length 474;

Best Local Similarity 27.2%; Pred. No. 5.5;

Matches 41; Conservative 22; Mismatches 50; Indels 38; Gaps 10;

Qy 68 VVGSTVPLSPKVDLVEKEVAGLWIKIPCTDYI-----GSCTFEH---FCDVLDM--- 117

Db 228 VIGERCPI-----VDTWQETGIMI-TPLCAISTKGSATLPPGILADIVDLEGN 281

Qy 118 LIPTGE-----PCPELRT-YGLP-----CHCPFKGTYSLPKSEFAPVDPLEL 159

Db 282 TVPENEGYLAVRYPFGMRVTYGDPERFRRTYLGTHPP-KDGNITYTFAGDGARKDEG 340

Qy 160 PSWLTGTVNRIEVSLSGKRLGCIKIAASL 190

Db 341 YFWMG---RVDDLNVSGHRLGTMEVESAL 368

RESULT 15

US-10-094-886-196

Sequence 196, Application US/10094886

Publication No. US20040002120A1

GENERAL INFORMATION:

APPLICANT: Kekuda, Ramesh

APPLICANT: Tchernev, Velizar T.

APPLICANT: Liu, Xiaohong

APPLICANT: Spytek, Kimberly A.

APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine

APPLICANT: Bernet, Corine A.

APPLICANT: Li, Li

APPLICANT: Gorman, Linda

APPLICANT: Malyankar, Uriel M.

APPLICANT: Boldog, Ferenc

APPLICANT: Guo, Xiaojia

APPLICANT: Shenoy, Suresh

APPLICANT: Padigaru, Muralidhara

APPLICANT: Taupier, Raymond J., Jr.

APPLICANT: Miller, Charles

APPLICANT: Casman, Stacie

APPLICANT: Pena, Carol

APPLICANT: Gangolli, Saha

APPLICANT: Gusev, Vladimir

APPLICANT: Smithson, Brynnda

APPLICANT: Zerhusen, Bryan

APPLICANT: Gerlach, Valerie

APPLICANT: Pochart, Pascal

APPLICANT: Fernandes, Elma

APPLICANT: Shimkets, Richard

APPLICANT: Rastelli, Luca

APPLICANT: Spaderna, Steven

APPLICANT: LaRochele, William

APPLICANT: Zhong, Mei

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS

FILE REFERENCE: 21402-290 B

CURRENT APPLICATION NUMBER: US/10/094,886

CURRENT FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: 60/274,322

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 60/313,182

PRIOR FILING DATE: 2001-08-17

PRIOR APPLICATION NUMBER: 60/288,052

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/318,510

PRIOR FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 60/274,281

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 60/314,018

PRIOR FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: 60/274,194

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: 60/274,849

PRIOR FILING DATE: 2001-03-09

PRIOR APPLICATION NUMBER: 60/296,693

PRIOR FILING DATE: 2001-06-07

PRIOR APPLICATION NUMBER: 60/313,626

PRIOR FILING DATE: 2001-08-21

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 298

SOFTWARE: Patentin 2.1

SEQ ID NO 196

LENGTH: 575

TYPE: PRT

ORGANISM: Homo sapiens

US-10-094-886-196

Query Match 8.4%; Score 86; DB 15; Length 575;

Best Local Similarity 23.6%; Pred. No. 7.1;

Matches 49; Conservative 23; Mismatches 76; Indels 60; Gaps 12;

Qy 8 PLLIALGLLIAT-----PAQAHLKPSQLSFSWDCNCFEGKDPAPVIRSLTLEPPDIV 59

Db 135 PLCVAVSAAEATVPSEPIWEEQCEVKADGFLCEHF-----PATCRPLAVEPGAAA 186

Qy 60 VPGNVLVS-----VGSTVPLSS-----PLKVDLVL-----EKEVAGLWIKI 97

Db 187 AAVSITYGTPFAARGAGFQALPVGSSAAVAPLGLQLMCTAPPAGVQGHWAREAFGAW--- 243

Qy 98 PCTDYIGSCTFEHFCVDLMDLPTGEBPCPEP-----LRTYGLPCHCPFKGTYSLPKSEFA 153

Db 244 DCSVENGGC--EHTCNA-----IPCAPRCQCPAGNALQADGRSCTASATQSCNDLCE-HFC 296

Qy 154 VPDLFSPSWLTGTVNRIEVSLSGKRL 181

Db 297 VPNDQP-----GSY---SCWCETGYRL 316

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Job time : 422.884 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 19:16:56 ; Search time 512.093 Seconds
(without alignments)
616.687 Million cell updates/sec

Title: US-10-030-937-9
Perfect score: 1018
Sequence: 1 MSLMQAPLIALGLLLATP.....LSSSGKRLGCIKIAASLKGI 193

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DSEXT=7

Database :

Issued Patents NA:*
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2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97.5	9.6	20966	4	US-09-776-976-7
2	97.5	9.6	20966	4	US-09-909-547-7
3	97.5	9.6	20966	4	US-09-569-852B-1
4	92.5	9.1	9950	4	US-09-949-016-12075
5	92.5	9.1	9950	4	US-09-949-016-14226
6	92	9.0	99748	4	US-09-949-016-11990
7	92	9.0	99749	4	US-09-949-016-16518
8	91	8.9	455726	4	US-09-949-016-14157
9	91	8.9	481115	4	US-09-949-016-11940
10	89.5	8.8	890	1	US-08-592-126-78
11	89.5	8.8	890	4	US-09-168-595-78
12	89.5	8.8	1633	1	US-07-866-979-5

ALIGNMENTS

RESULT 1

US-09-776-976-7
; Sequence 7, Application US/09776976
; Patent No. 6566332
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OEG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.US4.REG
; CURRENT APPLICATION NUMBER: US/09/776,976
; PRIOR FILING DATE: 2001-02-05
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 7
; LENGTH: 20966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..4811
; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: exon
; LOCATION: 4812..4851
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 15144..15365

Sequence 5, Appli
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Sequence 5, Appli
Sequence 5, Appli
Sequence 1343, Ap
Sequence 30962, A
Sequence 30963, A
Sequence 158143,
Sequence 158144,
Sequence 806, App
Sequence 12411, A
Sequence 16154, A
Sequence 13584, A
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Sequence 16110, A
Sequence 11934, A
Sequence 7, Appli
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Sequence 25, Appli
Sequence 83862, A
Patent No. 5466668
Patent No. 5466668
Sequence 13109, A
Sequence 3414, Ap

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; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 16277..20559
; OTHER INFORMATION: exon 3
; NAME/KEY: misc binding
; LOCATION: 20560..20966
; OTHER INFORMATION: 3' regulatory region
; NAME/KEY: allele
; LOCATION: 3787
; OTHER INFORMATION: 9-27-261 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 11118
; OTHER INFORMATION: 99-14387-129 : polymorphic base A or C
; NAME/KEY: allele
; LOCATION: 15120
; OTHER INFORMATION: 9-12-48 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15196
; OTHER INFORMATION: 9-12-124 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 15427
; OTHER INFORMATION: 9-12-355 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 15500
; OTHER INFORMATION: 9-12-428 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 15863
; OTHER INFORMATION: 99-14405-105 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 17170
; OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A
; NAME/KEY: primer_bind
; LOCATION: 3528..3545
; OTHER INFORMATION: 9-27.pu
; NAME/KEY: primer_bind
; LOCATION: 3928..3946
; OTHER INFORMATION: 9-27.rp complement
; NAME/KEY: primer_bind
; LOCATION: 10990..11008
; OTHER INFORMATION: 99-14387.pu
; NAME/KEY: primer_bind
; LOCATION: 11423..11442
; OTHER INFORMATION: 99-14387.rp complement
; NAME/KEY: primer_bind
; LOCATION: 15073..15092
; OTHER INFORMATION: 9-12.pu
; NAME/KEY: primer_bind
; LOCATION: 15503..15520
; OTHER INFORMATION: 9-12.rp complement
; NAME/KEY: primer_bind
; LOCATION: 15759..15776
; OTHER INFORMATION: 99-14405.pu
; NAME/KEY: primer_bind
; LOCATION: 16191..16211
; OTHER INFORMATION: 99-14405.rp complement
; NAME/KEY: primer_bind
; LOCATION: 16982..17001
; OTHER INFORMATION: 9-16.pu
; NAME/KEY: primer_bind
; LOCATION: 17384..17402
; OTHER INFORMATION: 9-16.rp complement
; NAME/KEY: misc_binding
; LOCATION: 3775..3799
; OTHER INFORMATION: 9-27-261.probe
; NAME/KEY: misc binding
; LOCATION: 11106..11130
; OTHER INFORMATION: 99-14387-129.probe
; NAME/KEY: misc binding
; LOCATION: 15108..15132
; OTHER INFORMATION: 9-12-48.probe
; NAME/KEY: misc binding
; LOCATION: 15184..15208
; OTHER INFORMATION: 9-12-124.probe

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; NAME/KEY: misc binding
; LOCATION: 15415..15439
; OTHER INFORMATION: 9-12-355.probe
; NAME/KEY: misc binding
; LOCATION: 15488..15512
; OTHER INFORMATION: 9-12-428.probe
; NAME/KEY: misc binding
; LOCATION: 15851..15875
; OTHER INFORMATION: 99-14405-105.probe
; NAME/KEY: misc binding
; LOCATION: 17158..17182
; OTHER INFORMATION: 9-16-189.probe
; NAME/KEY: primer_bind
; LOCATION: 3768..3786
; OTHER INFORMATION: 9-27-261.mis
; NAME/KEY: primer_bind
; LOCATION: 3788..3806
; OTHER INFORMATION: 9-27-261.mis complement
; NAME/KEY: primer_bind
; LOCATION: 11099..11117
; OTHER INFORMATION: 99-14387-129.mis
; NAME/KEY: primer_bind
; LOCATION: 11119..11137
; OTHER INFORMATION: 9-12-48.mis
; NAME/KEY: primer_bind
; LOCATION: 15101..15119
; OTHER INFORMATION: 9-12-48.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15121..15139
; OTHER INFORMATION: 9-12-124.mis
; NAME/KEY: primer_bind
; LOCATION: 15177..15195
; OTHER INFORMATION: 9-12-124.mis
; NAME/KEY: primer_bind
; LOCATION: 15197..15215
; OTHER INFORMATION: 9-12-124.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15408..15426
; OTHER INFORMATION: 9-12-355.mis
; NAME/KEY: primer_bind
; LOCATION: 15428..15446
; OTHER INFORMATION: 9-12-355.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15481..15499
; OTHER INFORMATION: 9-12-428.mis
; NAME/KEY: primer_bind
; LOCATION: 15501..15519
; OTHER INFORMATION: 9-12-428.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15844..15862
; OTHER INFORMATION: 99-14405-105.mis
; NAME/KEY: primer_bind
; LOCATION: 15864..15882
; OTHER INFORMATION: 99-14405-105.mis complement
; NAME/KEY: primer_bind
; LOCATION: 17151..17169
; OTHER INFORMATION: 9-16-189.mis
; NAME/KEY: primer_bind
; LOCATION: 17171..17189
; OTHER INFORMATION: 9-16-189.mis complement
; US-09-776-976-7

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Alignment Scores:	7.68	Length:	20966
Pred. No.:	97.50	Matches:	57
Score:	41.75%	Conservative:	24
Best Local Similarity:	29.38%	Mismatches:	72
Query Match:	9.58%	Indels:	41
DB:	4	Gaps:	10

US-10-030-937-9 (1-193) x US-09-776-976-7 (1-20966)

Qy 19 ThrProAlaGlnAla-----HisLeuLysLysProSerGlnLeuSerSer 33


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Db      6579 ACTCCAGCTGGCAAAAGACAACTCCATCTCAAAAAAATAAGACACA 6638
Qy      34 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeu 53
Db      6639 AGACTGGCTCCTTGTCTTTTGGGA-----CAGGGTCTCACTCTA 6680
Qy      54 GluProAspProIleValValProGlyAsnValThr-----LeuSerValVal 59
Db      6681 TCACCC---AGCTGGAGTGCAGTGGTGCATCACTGACGCTCAGATTTCCCA 6737
Qy      70 GlySerThrSerValProLeuSerSer-ProLeuLysValAspLeuValLeuGluLysG1 89
Db      6738 GGCTCAAGTACCTCCATCTAGCTCTGAGTACCTGGGACTACAGGTGTGTCAC 6797
Qy      89 uValLaGlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheG1 109
Db      6798 CATGCTGGCTAAATTTTAAAAATTTTGTAGAGATGAGGTCTCACTA----- 6846
Qy      109 uHisPheCysAspValLeuAspMetLeuIleProThrGlyGluProCysProGluProLe 129
Db      6847 -TATTGGCTGGGGGCTCAAACTCTCGGCTCAGCAGTCTCCCA---CCTCAGCCTCC 6902
Qy      129 uArgThrTyrGlyLeu---ProCysHis-----CysProPheLysGluGlyTh 144
Db      6903 CAAAAGCTGGGATATATGCTTCTTTTAAGTGGCTGTAGGACAAACTTTCAC 6962
Qy      144 rTyrSerLeuProLys-SerGluPheAlaValProAspLeuGluLeuProSer----- 161
Db      6963 CTACTCTTGTCAAGCAGTGGACCGTGTCCAGACATACCGCTAAAGTCAAGAGTG 7022
Qy      162 -----TrpLeuThrGlyAsnTyrArgIleGluSerValLeuSerSerGlyL 179
Db      7023 ATGCTCTTTGGAGAGATACTTTCAATCAGGAATTTCAATCAGAAATTCATCATGTGGAG 7082
Qy      179 yeaGleu-----GlyCys 183
Db      7083 AGAGACTTATCTTAAAAATGTGGTGGTGGGATGC 7120

RESULT 2
US-09-547-7
; Sequence 7, Application US/0909547
; Patent No. 6579852
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: OEG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76.US6.CIP
; CURRENT APPLICATION NUMBER: US/09/909,547
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/776,976
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 7
; LENGTH: 20966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..4811
; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: exon
; LOCATION: 4812..4851
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 15144..15365
; OTHER INFORMATION: exon 2
; NAME/KEY: exon
; LOCATION: 16277..20559
; OTHER INFORMATION: exon 3
; NAME/KEY: misc feature
; LOCATION: 20560..20966
; OTHER INFORMATION: 3' regulatory region
; NAME/KEY: allele
; LOCATION: 3787
; OTHER INFORMATION: 9-27-261 : polymorphic base G or C
; NAME/KEY: allele
; LOCATION: 11118
; OTHER INFORMATION: 99-14387-129 : polymorphic base A or C
; NAME/KEY: allele
; LOCATION: 15120
; OTHER INFORMATION: 9-12-48 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 15196
; OTHER INFORMATION: 9-12-124 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 15427
; OTHER INFORMATION: 9-12-355 : polymorphic base G or T
; NAME/KEY: allele
; LOCATION: 15500
; OTHER INFORMATION: 9-12-428 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 15863
; OTHER INFORMATION: 99-14405-105 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 17170
; OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A
; NAME/KEY: primer bind
; LOCATION: 3528..3545
; OTHER INFORMATION: 9-27.pu
; NAME/KEY: primer bind
; LOCATION: 3928..3946
; OTHER INFORMATION: 9-27.rp complement
; NAME/KEY: primer bind
; LOCATION: 10990..11008
; OTHER INFORMATION: 99-14387.pu
; NAME/KEY: primer bind
; LOCATION: 11423..11442
; OTHER INFORMATION: 99-14387.rp complement
; NAME/KEY: primer bind
; LOCATION: 15073..15092
; OTHER INFORMATION: 9-12.pu
; NAME/KEY: primer bind
; LOCATION: 15503..15520
; OTHER INFORMATION: 9-12.rp complement
; NAME/KEY: primer bind
; LOCATION: 15759..15776
; OTHER INFORMATION: 99-14405.pu
; NAME/KEY: primer bind
; LOCATION: 16191..16211
; OTHER INFORMATION: 99-14405.rp complement
; NAME/KEY: primer bind
; LOCATION: 16982..17001
; OTHER INFORMATION: 9-16.pu
; NAME/KEY: primer bind
; LOCATION: 17384..17402
; OTHER INFORMATION: 9-16.rp complement
; NAME/KEY: misc binding
; LOCATION: 3775..3799
; OTHER INFORMATION: 9-27-261.probe
; NAME/KEY: misc binding
; LOCATION: 11106..11130
; OTHER INFORMATION: 99-14387-129.probe
; NAME/KEY: misc binding
; LOCATION: 15108..15132
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OTHER INFORMATION: 9-12-48.probe
NAME/KEY: misc.binding
LOCATION: 15184..15208
OTHER INFORMATION: 9-12-124.probe
NAME/KEY: misc.binding
LOCATION: 15415..15439
OTHER INFORMATION: 9-12-355.probe
NAME/KEY: misc.binding
LOCATION: 15488..15512
OTHER INFORMATION: 9-12-428.probe
NAME/KEY: misc.binding
LOCATION: 15851..15875
OTHER INFORMATION: 99-14405-105.probe
NAME/KEY: misc.binding
LOCATION: 17158..17182
OTHER INFORMATION: 9-16-189.probe
NAME/KEY: primer.bind
LOCATION: 3768..3786
OTHER INFORMATION: 9-27-261.mis
NAME/KEY: primer.bind
LOCATION: 3788..3806
OTHER INFORMATION: 9-27-261.mis complement
NAME/KEY: primer.bind
LOCATION: 11099..11117
OTHER INFORMATION: 99-14387-129.mis
NAME/KEY: primer.bind
LOCATION: 11119..11137
OTHER INFORMATION: 99-14387-129.mis complement
NAME/KEY: primer.bind
LOCATION: 15177..15195
OTHER INFORMATION: 9-12-124.mis
NAME/KEY: primer.bind
LOCATION: 15197..15215
OTHER INFORMATION: 9-12-124.mis complement
NAME/KEY: primer.bind
LOCATION: 15408..15426
OTHER INFORMATION: 9-12-355.mis
NAME/KEY: primer.bind
LOCATION: 15428..15446
OTHER INFORMATION: 9-12-355.mis complement
NAME/KEY: primer.bind
LOCATION: 15481..15499
OTHER INFORMATION: 9-12-428.mis
NAME/KEY: primer.bind
LOCATION: 15501..15519
OTHER INFORMATION: 9-12-428.mis complement
NAME/KEY: primer.bind
LOCATION: 15844..15862
OTHER INFORMATION: 99-14405-105.mis
NAME/KEY: primer.bind
LOCATION: 15864..15882
OTHER INFORMATION: 99-14405-105.mis complement
NAME/KEY: primer.bind
LOCATION: 17151..17169
OTHER INFORMATION: 9-16-189.mis
NAME/KEY: primer.bind
LOCATION: 17171..17189
OTHER INFORMATION: 9-16-189.mis complement
US-09-909-547-7
Alignment Scores:
Pred. No.: 7.68 Length: 20966
Score: 97.50 Matches: 57
Percent Similarity: 41.75% Conservative: 24
Best Local Similarity: 29.38% Mismatches: 72
Query Match: 9.58% Indels: 41
DB: 4 Gaps: 10
```

US-10-030-937-9 (1-193) x US-09-909-547-7 (1-20966)

QY 19 ThrProAlaGlnAla-----HisLeuLysLysProSerGlnLeuSerSer 33
|||||
Db 6579 ACTCCAGCCTGGGCAAAAAGACAAATCCATCTCAAAAAAATAAGACACA 6638
QY 34 PheSerTrpAsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeu 53
|||||
Db 6639 AGACTGGCTCCTTGTCTTTTGGGA-----CAGGGTCTCACTCTA 6680
QY 54 GluProAspProIleValProGlyAsnValThr-----LeuSerValVal 69
|||||
Db 6681 TCACCC---AGGCTGGAGTGCAGTGTGCAATCACAGCTCACTGCAGCCTCGATTTCCCA 6737
QY 70 GlySerThrSerValProLeuSerSer-ProLeuLysValAspLeuValLeuLysG1 89
|||||
Db 6738 GGCTCAAGTGACCCCTCCCATTTAGCCTCCTGAGTAGCTGGGACTACAGGTGTGTCAAC 6797
QY 89 uValAlaGlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheG1 109
|||||
Db 6798 CATGCTGGCTAATTTTAAAAATTTTGTAGAGATGAGTCTCACTA----- 6846
QY 109 uHisPheCysAspValLeuAspMetLeulleProThrGlyGluProCysProGluProLe 129
|||||
Db 6847 -TATTGGCTGGGGGGCCTCAAACTCCTGGGCTCAGCAGTCTCTCCCA---CCTCAGCCTCC 6902
QY 129 uArgThrTyrGlyLeu---ProCysHis-----CysProPheLysGluGlyTh 144
|||||
Db 6903 CAAAAGGCTGGGATATATGCTTGTCTTTTAAGGTGGCTGAGGACAAACTTTCCAC 6962
QY 144 rTyrSerLeuProLys-SerGluPheAlaValProAspLeuGluLeuProSer----- 161
Db 6963 CTACTCTTGTCAAGCCAGTGGACCGTGTGCCAGACATACGGCTAAAGTCAAGAGGTG 7022
QY 162 -----TrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyL 179
Db 7023 ATGTCCTTTTGGAGAGATACTTTCAATCAGGAATTTCAATCAGAAATTCATATCATGTGGAG 7082
QY 179 ysArgLeu-----GlyCys 183
Db 7083 AGAGACTTATCTCTAAATAATGTGGTGTGGTGGATGC 7120

RESULT 3
US-09-569-852B-1
; Sequence 1, Application US/09569852B
; Patent No. 6582909
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Denison, Blake
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: APMI Biallelic Markers and Uses Thereof
; FILE REFERENCE: GEN-T113XC2
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/IB99/01858
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 09/434,848
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 60/119,593
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/107,113
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 20966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4811)

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; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: primer_bind
; LOCATION: (14683)..(14701)
; OTHER INFORMATION: 17-34-860.mis
; NAME/KEY: primer_bind
; LOCATION: (14703)..(14721)
; OTHER INFORMATION: 17-34-860.mis complement
; NAME/KEY: primer_bind
; LOCATION: (14738)..(14756)
; OTHER INFORMATION: 17-34-915.mis
; NAME/KEY: primer_bind
; LOCATION: (14758)..(14776)
; OTHER INFORMATION: 17-34-915.mis complement
; NAME/KEY: primer_bind
; LOCATION: (14796)..(14814)
; OTHER INFORMATION: 17-35-71.mis
; NAME/KEY: primer_bind
; LOCATION: (14816)..(14834)
; OTHER INFORMATION: 17-35-71.mis complement
; NAME/KEY: primer_bind
; LOCATION: (15031)..(15049)
; OTHER INFORMATION: 17-35-306.mis
; NAME/KEY: primer_bind
; LOCATION: (15051)..(15069)
; OTHER INFORMATION: 17-35-306.mis complement
; NAME/KEY: primer_bind
; LOCATION: (15101)..(15119)
; OTHER INFORMATION: 9-12-48.mis
; NAME/KEY: primer_bind
; LOCATION: (15121)..(15139)
; OTHER INFORMATION: 9-12-48.mis complement
; NAME/KEY: primer_bind
; LOCATION: (15177)..(15195)
; OTHER INFORMATION: 9-12-124.mis
; NAME/KEY: primer_bind
; LOCATION: (15197)..(15215)
; OTHER INFORMATION: 9-12-124.mis complement
; NAME/KEY: primer_bind
; LOCATION: (15408)..(15426)
; OTHER INFORMATION: 9-12-355.mis
; NAME/KEY: primer_bind
; LOCATION: (15428)..(15446)
; OTHER INFORMATION: 9-12-355.mis complement
; NAME/KEY: primer_bind
; LOCATION: (15481)..(15499)
; OTHER INFORMATION: 9-12-428.mis
; NAME/KEY: primer_bind
; LOCATION: (15501)..(15519)
; OTHER INFORMATION: 9-12-428.mis complement
; NAME/KEY: primer_bind
; LOCATION: (15661)..(15679)
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; NAME/KEY: primer_bind
; LOCATION: (15681)..(15699)
; OTHER INFORMATION: 17-36-47.mis complement
; NAME/KEY: primer_bind
; LOCATION: (15771)..(15789)
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; NAME/KEY: primer_bind
; LOCATION: (15791)..(15809)
; OTHER INFORMATION: 17-36-120.mis complement
; NAME/KEY: primer_bind
; LOCATION: (15844)..(15862)
; OTHER INFORMATION: 99-14405-105.mis
; NAME/KEY: primer_bind
; LOCATION: (15864)..(15882)
; OTHER INFORMATION: 99-14405-105.mis complement
; NAME/KEY: primer_bind
; LOCATION: (17151)..(17169)
; OTHER INFORMATION: 9-16-189.mis
; NAME/KEY: primer_bind
; LOCATION: (17171)..(17189)
; OTHER INFORMATION: 9-16-189.mis complement

; NAME/KEY: primer_bind
; LOCATION: (17810)..(17828)
; OTHER INFORMATION: 17-37-629.mis
; NAME/KEY: primer_bind
; LOCATION: (17830)..(17848)
; OTHER INFORMATION: 17-37-629.mis complement
; NAME/KEY: primer_bind
; LOCATION: (17992)..(18010)
; OTHER INFORMATION: 17-37-811.mis
; NAME/KEY: primer_bind
; LOCATION: (18012)..(18030)
; OTHER INFORMATION: 17-37-811.mis complement
; NAME/KEY: primer_bind
; LOCATION: (18470)..(18488)
; OTHER INFORMATION: 17-38-349.mis
; NAME/KEY: primer_bind
; LOCATION: (18490)..(18508)
; OTHER INFORMATION: 17-38-349.mis complement
; NAME/KEY: primer_bind
; LOCATION: (926)..(944)
; OTHER INFORMATION: 17-30-216.mis
; NAME/KEY: primer_bind
; LOCATION: (946)..(964)
; OTHER INFORMATION: 17-30-216.mis complement
; NAME/KEY: primer_bind
; LOCATION: (3719)..(3737)
; OTHER INFORMATION: 9-27-211.mis
; NAME/KEY: primer_bind
; LOCATION: (3739)..(3757)
; OTHER INFORMATION: 9-27-211.mis complement
; NAME/KEY: primer_bind
; LOCATION: (3754)..(3772)
; OTHER INFORMATION: 9-27-246.mis
; NAME/KEY: primer_bind
; LOCATION: (3774)..(3792)
; OTHER INFORMATION: 9-27-246.mis complement
; NAME/KEY: primer_bind
; LOCATION: (3768)..(3786)
; OTHER INFORMATION: 9-27-261.mis
; NAME/KEY: primer_bind
; LOCATION: (3788)..(3806)
; OTHER INFORMATION: 9-27-261.mis complement
; NAME/KEY: primer_bind
; LOCATION: (5076)..(5094)
; OTHER INFORMATION: 17-31-298.mis
; NAME/KEY: primer_bind
; LOCATION: (5096)..(5114)
; OTHER INFORMATION: 17-31-298.mis complement
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; LOCATION: (5191)..(5209)
; OTHER INFORMATION: 17-31-413.mis
; NAME/KEY: primer_bind
; LOCATION: (5211)..(5229)
; OTHER INFORMATION: 17-31-413.mis complement
; NAME/KEY: primer_bind
; LOCATION: (5364)..(5385)
; OTHER INFORMATION: 17-31.rp complement
; NAME/KEY: primer_bind
; LOCATION: (10618)..(10636)
; OTHER INFORMATION: 17-32-24.mis
; NAME/KEY: primer_bind
; LOCATION: (10638)..(10656)
; OTHER INFORMATION: 17-32-24.mis complement
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; OTHER INFORMATION: 99-14387-50.mis
; NAME/KEY: primer_bind
; LOCATION: (11040)..(11058)
; OTHER INFORMATION: 99-14387-50.mis complement
; NAME/KEY: primer_bind
; LOCATION: (11099)..(11117)
; OTHER INFORMATION: 99-14387-129.mis
; NAME/KEY: primer_bind
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/ LOCATION: (11119)..(11137)
/ OTHER INFORMATION: 99-14387-129.mis complement
/ NAME/KEY: primer_bind
/ LOCATION: (11169)..(11187)
/ OTHER INFORMATION: 99-14387-199.mis
/ NAME/KEY: primer_bind
/ LOCATION: (11189)..(11207)
/ OTHER INFORMATION: 99-14387-199.mis complement
/ NAME/KEY: primer_bind
/ LOCATION: (13954)..(13972)
/ OTHER INFORMATION: 17-33-TGAGACT.mis
/ NAME/KEY: primer_bind
/ LOCATION: (13974)..(13992)
/ OTHER INFORMATION: 17-33-TGAGACT.mis complement
/ NAME/KEY: exon
/ LOCATION: (4812)..(4851)
/ OTHER INFORMATION:
/ NAME/KEY: exon
/ LOCATION: (15144)..(15365)
/ OTHER INFORMATION:
/ NAME/KEY: exon
/ LOCATION: (16277)..(20559)
/ OTHER INFORMATION:
/ NAME/KEY: misc_feature
/ LOCATION: (20560)..(20966)
/ OTHER INFORMATION: 3' regulatory region
```

```
Alignment Scores:
Pred. No.: 7.68 Length: 20966
Score: 97.50 Matches: 57
Percent Similarity: 41.75% Conservative: 24
Best Local Similarity: 29.38% Mismatches: 72
Query Match: 9.58% Indels: 41
DB: 4 Gaps: 10
```

US-10-030-937-9 (1-193) x US-09-569-852B-1 (1-20966)

```
Qy 19 ThrProAlaGlnAla-----HisLeuLysLysProSerGlnLeuSerSer 33
Db 6579 ACTCAGCCTGGGCAAAAGAGCAAAACTCATCTCAAAAAAAAAAAAAAAAAATAGACACA 6638
Qy 34 PheSerTrpAspAenCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeu 53
Db 6639 AGACTGGCTCCTGCTCTCTTTTGGGA-----CAGGGCTCTCACTCTA 6680
Qy 54 GluProAspProIleValProGlyAsnValThr-----LeuSerValVal 69
Db 6681 TCACCC---AGGCTGGAGTGCAGTGGTGCATCACTACAGCTCAGCCTCGATTCCCA 6737
Qy 70 GlySerThrSerValProLeuSerSer-ProLeuLysValAspLeuValLeuGlyLysG1 89
Db 6738 GGCTCAAGTGACCTCCCATCTTAGCCTCCTGAGTAGCTGGACTACAGGTGTGTGCAAC 6797
Qy 89 uValAlaGlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheG1 109
Db 6798 CATGCTGGCTGAATTTTAAAAATTTTGTAGAGATGAGGTCTCACTA----- 6846
Qy 109 uHisPheCysAspValLeuAspMetLeuIleProThrGlyGluProCysProGluProLe 129
Db 6847 -TATTGGCTGGGGGCTCAAACTCCTGGGTCTACAGCTCCTCCCA---CCTAGCCTCC 6902
Qy 129 uArgThrTyrGlyLeu---ProCysHis-----CysProPheLysGluGlyTh 144
Db 6903 CAAAAGCTGGATATATGCTTCTTTTAAGTGGCTGTAGGACAACTTTCCAC 6962
Qy 144 rTySerLeuProLys-SerGluPheAlaValProAspLeuGluLeuProSer----- 161
Db 6963 CTACTCTTGTCAAGCCAGTGGCGGTGGTCCAGACATACGGCTAAAGTCAAGAGGTG 7022
Qy 162 -----TrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyL 179
Db 7023 ATGCTCTTTGGAGAGATACTTTCAATCAGGAATTTCAATCAGGAATTTCAATCATGTGTGAG 7082
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Qy 179 ysArgLeu-----GlyCys 183
Db 7083 AGAGACTTATCCTAAAAATGTGTGGTGGGTGGATGC 7120
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RESULT 4

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US-09-949-016-12075
; Sequence 12075, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12075
; LENGTH: 9950
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12075
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Alignment Scores:
Pred. No.: 9.26 Length: 9950
Score: 92.50 Matches: 50
Percent Similarity: 36.53% Conservative: 30
Best Local Similarity: 22.83% Mismatches: 78
Query Match: 9.09% Indels: 61
DB: 4 Gaps: 11
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US-10-030-937-9 (1-193) x US-09-949-016-12075 (1-9950)

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Qy 4 LeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAlaGlnAla 23
Db 4397 CTCTTCTCTCCCTCCCTCTGTC-----ACCTCCCT 4426
Qy 24 HisLeuLysLysProSerGlnLeu-----SerSerPheSerTrpAsp 37
Db 4427 AACTATGGGTCCCAACACAGGTTCTCGGCAGCAGGTGGCTACGTATTGCTGGTGC 4486
Qy 38 AsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspPro 57
Db 4487 TCACGTGTC-----GACCCCTTTATATTCTGCGACGCTCACAGCTGCCATCACC 4537
Qy 58 IleValVal----- 60
Db 4538 CTCTTCTCTCTCCGGTGGCTTCCAGCGTCATTCGGGCTTCCCTCTCTCTCCGCTA 4597
Qy 61 ---ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerPro 79
Db 4598 AGCCCACTTCTGGGTTTCTGAGCCTCTCAGCTCATCA-----CCTATTCTGCTCCT 4651
Qy 80 -----LeuLysValAspLeuValLeuGlyLysGluValAlaGlyLeuTrpIleLys 96
Db 4652 TAGCACTCTTATGAGCCAGACCATCTCTCTGAATTTCTTCTGCTCTC----- 4696
Qy 97 IleProCysThrAspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAsp 116
Db 4697 CTTCCTTGACGCCCACTCCTCTCC---CCACTGCAGCACCCAGCTTTAACTTTGGGT 4753
Qy 117 MetLeuIleProThrGlyGluProCysProGluProLeuArgThrTyr----- 132
Db 4754 TTCTCTTCTCTCAGGTCTGGAGCCCCCAACTCCCTTGACAGGTACGCTGGAGCAGGT 4813
Qy 133 -----GlyLeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProLys 149
```

Db 4814 TCAGGGTGGGCTGCCCTGCCCTGCTGGTGGTGGGACCGGCTTTCCTCACT 4873
Qy 150 SerGluPheAlaValProAspLeuGluLeuProSerTrpLeuThrTrpGlyAsn----- 167
Db 4874 GCCAAGTGGACTCCTCCTGGG---GGAGGCCCTGACCTCTCGTGTACTGGAGACAATGGC 4930
Qy 168 -----TyrArgIleGluSerValLeuSerSerGlyLysArgLeuGlyCys 183
Db 4931 GACTTTACCTTCGACTAGAGGATGTAGCCAGCCAGCGCTGGGACCTACACCTGC 4987

RESULT 5
US-09-949-016-14226
; Sequence 14226 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14226
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14226

Alignment Scores:
Pred. No.: 9,26 Length: 9950
Score: 92.50 Matches: 50
Percent Similarity: 36.53% Conservative: 30
Best Local Similarity: 22.83% Mismatches: 78
Query Match: 9.09% Indels: 61
DB: 4 Gaps: 11

US-10-030-937-9 (1-193) x US-09-949-016-14226 (1-9950)
Qy 4 LeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAlaGlnAla 23
Db 4397 CTCCTTCCTGCCCTCCTGTC-----ACCTCCCT 4426

Qy 24 HisLeuLysLysProSerGlnLeu-----SerSerPheSerTrpAsp 37
Db 4427 AACTATGGGTCCCAACACGAGTCTCGGACGAGTGGCTACGTTCATTGTGGTGC 4486

Qy 38 AsnCysPheGluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspPro 57
Db 4487 TCACTGTC-----GACCCCTTTATATTGCTGGCAGCCTCACAGTGCATCACCC 4537

Qy 58 IleValVal----- 60
Db 4538 CTCTCTGCTTCCTCCGTGGCTTCAGCGTCATTGGCGGCTTCCTCTCCTTCGGGTA 4597

Qy 61 ---ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerPro 79
Db 4598 AGCCCACTGTCTGGTGTCTGAGCCTCCTCAGCTCATCA-----CCTTATTCTGCTCT 4651

Qy 80 -----LeuLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLys 96
Db 4652 TAGCACTTTATAGCCAGACCATCTCCTGAATCTTCTGCCTCC----- 4696

Qy 97 IleProCysThrAspTrpIleGlySerCysThrPheGluHisPheCysAspValLeuAsp 116
Db 4697 CTTCCTTGAGCCCGCAGCACTCCTCC---CCACTGACGACCCAGCTTAACTTTGGT 4753

Qy 117 MetLeuIleProThrGlyGluProCysProGluProLeuArgThrTyr----- 132
Db 4754 TTTCTTTTCTCTCAGGTCTGGAGCCCCCACTCCCTTACAGTGTACCTGGAGCAGGT 4813
Qy 133 -----GlyLeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProLys 149
Db 4814 TCAGGGTGGGCTGCCCTGCCCTGCTGTGTGGGACCGGCTTTCCTCACT 4873
Qy 150 SerGluPheAlaValProAspLeuGluLeuProSerTrpLeuThrTrpGlyAsn----- 167
Db 4874 GCCAAGTGGACTCCTCCTGGG---GGAGGCCCTGACCTCTCGTGTACTGGAGACAATGGC 4930

Qy 168 -----TyrArgIleGluSerValLeuSerSerGlyLysArgLeuGlyCys 183
Db 4931 GACTTTACCTTCGACTAGAGGATGTAGCCAGCCAGCGCTGGGACCTACACCTGC 4987

RESULT 6
US-09-949-016-11990
; Sequence 11990 Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11990
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11990

Alignment Scores:
Pred. No.: 505 Length: 99748
Score: 92.00 Matches: 52
Percent Similarity: 40.22% Conservative: 22
Best Local Similarity: 28.26% Mismatches: 56
Query Match: 9.04% Indels: 54
DB: 4 Gaps: 12

US-10-030-937-9 (1-193) x US-09-949-016-11990 (1-99748)
Qy 5 MetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAlaGlnAlaHis 24
Db 77933 CTGGCCTCACCTCCTCTGGTCTCGTCTGCTCCTCTCCAGCCTCACCTCTCTGGTT--- 77989

Qy 25 LeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPheGluGlyLysAsp 44
Db 77990 -----CCTCGGTCACTCTCTCCAGCCTCA-----CCC 78016

Qy 45 ProAlaValIleArgSerLeuThrLeuGluProAspProIleValValProGlyAsnVal 64
Db 78017 CCTCGGTTCCTCGCTCACTCTCTGCGCTCACCTCCTCTG---ATTCTGCTCCTC 78073

Qy 65 -----ThrLeuSerValValGlySerThrSerVal 74
Db 78074 TCTCCAGCTTACCCCTCCGCTTCTCGTCTCACTATCTCCAGTCTCAACCTCTCTGGTT 78133

Qy 75 Pro-LeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAlaGlyLeu 94
Db 78134 CTGGCTCACTTCTCCAGCCTCCTG-----GCTCTTCACTCT 78172

Qy 94 rpIleValValProCysThrAspTrp---IleGlySerCys-----ThrPheGluH 110
Db 94 rpIleValValProCysThrAspTrp---IleGlySerCys-----ThrPheGluH 110

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Db 78173 GCTGACACACCGGTGATTCTTCANGAACCTGGCATGTGCCATTCCCTCTGCCAGGAAC 78232
Qy 110 isPheCysAspValLeuAspMetLeuileProThr-----GlyGluProCysProG 127
Db 78233 ATTTC-----CTCCCAAGCCTCCCATGGCTCACTCTGCCTG 78271
Qy 127 luProLeuArgThrTyGlyLeuProCysHisCysProPheLysGluGlyThrTySerL 147
Db 78272 TACACTGGCCCCACTGTCTGCTGCCAC---CCTGCTAGGTTCTCTCTAGTCCT 78328
Qy 147 euProLysSerGluPheAlaVal-----ProAspLeu-----GluLeuP 160
Db 78329 TGGCACCATCAGACACAGCACTGTGCACCCCTGAGCTGATCTCCCTGCCAGTCAGCTCC 78388
Qy 160 roSerTrp 162
Db 78389 CAGGGTGG 78396
RESULT 7
US-09-949-016-16518
; Sequence 16518, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16518
; LENGTH: 99749
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16518
Alignment Scores:
Pred. No.: 505 Length: 99749
Score: 92.00 Matches: 52
Percent Similarity: 40.22% Conservative: 22
Best Local Similarity: 28.26% Mismatches: 56
Query Match: 9.04% Indels: 54
DB: 4 Gaps: 12
US-10-030-937-9 (1-193) x US-09-949-016-16518 (1-99749)
Qy 5 MetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAlaGlnAlaHis 24
Db 77933 CTGGCCTCACCTCTCTGGTCTCTGGTCTCTCCAGCCTCACCTCTCTGGTT--- 77989
Qy 25 LeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPheGluGlyLysAsp 44
Db 77990 -----CCTCGGTCACTCTCTCCAGCCTCA-----CCC 78016
Qy 45 ProAlaValIleArgSerLeuThrLeuGluProAspProIleValValProGlyAsnVal 64
Db 78017 CCTCTGGTTCTCTGCTCACTCTCTCTGGCCTCACCTCTCTG---ATTCTGGCTCACTC 78073
Qy 65 -----ThrLeuSerValValGlySerThrSerVal 74
Db 78074 TCTCAGCTTCACCCCTCCGGTTCTCTCGTCACTATCTCCAGTCTCAACCTCTCTGGTT 78133
Qy 75 Pro--LeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAlaGlyLeuT 94
Db 78134 CCTGGCTCACTTCTCCAGCCTCACTG-----GCCTCTTCACTGT 78172
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Qy 94 rPileLysIleProCysThrAspTyr---IleGlySerCys-----ThrPheGluH 110
Db 78173 GCTGACACACCGGTGATTCTTCANGAACCTGGCATGTGCCATTCCCTCTGCCAGGAAC 78232
Qy 110 isPheCysAspValLeuAspMetLeuileProThr-----GlyGluProCysProG 127
Db 78233 ATTTC-----CTCCCAAGCCTCCCATGGCTCACTCTGCCTG 78271
Qy 127 luProLeuArgThrTyGlyLeuProCysHisCysProPheLysGluGlyThrTySerL 147
Db 78272 TACACTGGCCCCACTGTCTGCTGCCAC---CCTGCTAGGTTCTCTCTAGTCCT 78328
Qy 147 euProLysSerGluPheAlaVal-----ProAspLeu-----GluLeuP 160
Db 78329 TGGCACCATCAGACACAGCACTGTGCACCCCTGAGCTGATCTCCCTGCCAGTCAGCTCC 78388
Qy 160 roSerTrp 162
Db 78389 CAGGGTGG 78396
RESULT 8
US-09-949-016-14157/c
; Sequence 14157, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14157
; LENGTH: 455726
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(455726)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14157
Alignment Scores:
Pred. No.: 8,53e+03 Length: 455726
Score: 91.00 Matches: 51
Percent Similarity: 37.50% Conservative: 21
Best Local Similarity: 26.56% Mismatches: 77
Query Match: 8.94% Indels: 44
DB: 4 Gaps: 7
US-10-030-937-9 (1-193) x US-09-949-016-14157 (1-455726)
Qy 2 GlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAla 21
Db 103381 CAGAGCCTTCAGTCTCTCACCCCTCTGCTCTCTCTCTATCATGAAGCCACACAGCC 103322
Qy 22 GlnAlaHisLeuLysLysProSerGlnLeu---SerSerPheSerTrpAspAsn----- 38
Db 103321 TCTCACCCGGAAGAGCAGCCCGCCAGGCCCTCGAGCCTCTCTCTCATCGAACATACCCCA 103262
Qy 39 ---CysPheGluGlyLysAspProAlaValIleArgSerLeuThr----- 52
Db 103261 CAGTGTGGCAGAGCCCTGGCTCCACTTCCACACAGCCCCCTCTCTCACTCCACAGCC 103202
Qy 53 ---LeuGluProAspProIleVal-ValProGlyAsnValThrLeuSerValValGlySe 71
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Db 103201 TGAACGGGCGGCGACACAGCTCTGTTCTGCGCAAGGCCACGATG----- 103156
Qy 71 rThrSerValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAl 91
Db 103155 -ACTTCAGG-CTGTTCTCAAGTGGCCTTTCTGATGACACTTTGGCCACCTCACCTCTGGG 103098
Qy 91 aGlyLeuTrpIleValProCysThrAspTyrIleGlySerCysThrPheGluHisPh 111
Db 103097 GCACGGTGGCCCTCACTCCAGGGTGGCCACCTGCTCTCCACCCTCTCTCCAG----- 103043
Qy 111 eCysAspValLeuAspMetLeuProThrGlyGluProCys- ProGluProLeuArgT 131
Db 103042 -----CTCCTGGCGAGGGCCCTGCTCCCGACCCCTTGCCT 103005
Qy 131 hr-----TyrGlyLeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProL 149
Db 103004 GTGGGTTCTCGGGTCCCTCCACATATCCACAGGGACCTCACCTCTGCGCATGCCAA 102945
Qy 149 ysSerGluPheAlaValProAspLeuLeu----- 159
Db 102944 TGAACCTCCAAATTCGTATCCATCTCCAGGGCTCCCTTCTCTGAGCCCAACACCCACAC 102885
Qy 160 -----ProSerTrpLeuThr 164
Db 102884 CCACACCCACCGGGTCCACCTGCTGACC 102853

RESULT 9
US-09-949-016-11940/c
; Sequence 11940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11940
; LENGTH: 481115
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(481115)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-11940

Alignment Scores:
Pred. No.: 9.34e+03 Length: 481115
Score: 91.00 Matches: 51
Percent Similarity: 37.50% Conservative: 21
Best Local Similarity: 26.56% Mismatches: 77
Query Match: 8.94% Indels: 44
DB: 4 Gaps: 7

US-10-030-937-9 (1-193) x US-09-949-016-11940 (1-481115)

Qy 2 GlnSerIleuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrProAla 21
Db 80770 CAGAGCGCTTCAGTTCACCCCTCTGCTCTCTATCATGAAGCCACACCCAGCC 80711
Qy 22 GlnAlaHisLeuLysProSerGlnLeu---SerSerPheSerTrpAspAsn----- 38
Db 80710 TCTCACCGGAAAGCAGCAGCCCGAGGCGCTGCGAGCTCTGCTCCATCGGACATACCCCA 80651
```

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Qy 39 ---CysPheGluGlyLysAspProAlaValIleArgSerLeuThr----- 52
Db 80650 CAGTGGGCGCAAGGCTGCGTCCACTTCCACAGACCCCTCTCTACTCCCACTGCAGCC 80591
Qy 53 ---LeuGluProAspProIleVal-ValProGlyAsnValThrLeuSerValValGlySe 71
Db 80590 TCACTCCGCGCCGACACAGCTCTGTCTCTGCAAGGCCACGATG----- 80545
Qy 71 rThrSerValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAl 91
Db 80544 -ACTTCAGG-CTGTTCTCAAGTGGCCTTTCTGATGACACTTTGGCCACCTCACCTCTGGG 80487
Qy 91 aGlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheGluHisPh 111
Db 80486 GCACGGTGGCCCTCACTCCAGGGTGGCCACCTGCTCTCCACCCTCTCTCCAG----- 80432
Qy 111 eCysAspValLeuAspMetLeuIleProThrGlyGluProCys- ProGluProLeuArgT 131
Db 80431 -----CTCCTGGCGAGGGCCCTGCTCCCGACCCCTTGCCT 80394
Qy 131 hr-----TyrGlyLeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProL 149
Db 80393 GTGGGTTCTCGGGTCCCTCCACATATCCACAGGGACCTCACCTCTGCGCATGCCAA 80334
Qy 149 ysSerGluPheAlaValProAspLeuLeu----- 159
Db 80333 TGAACCTCCAAATTCGTATCCATCTCCAGGGCTCCCTTCTCTGAGCCCAACACCCACAC 80274
Qy 160 -----ProSerTrpLeuThr 164
Db 80273 CCACACCCACCGGGTCCACCTGCTGACC 80242

RESULT 10
US-08-592-126-78
; Sequence 78, Application US/08592126
; Patent No. 5921091
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 151
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,126
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 890 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: G256.seq
US-08-592-126-78

Alignment Scores:
Pred. No.: 0.386 Length: 890
Score: 89.50 Matches: 53
Percent Similarity: 39.89% Conservative: 22
Best Local Similarity: 28.19% Mismatches: 67
Query Match: 8.79% Indels: 47
DB: 1 Gaps: 10

US-10-030-937-9 (1-193) x US-08-592-126-78 (1-890)
Qy 3 SerLeuMetGlnAlaProLeuLeuLeuAlaLeuGlyLeuLeuAlaThrProAlaGln 22
Db 49 TCCTTTTACCAAAAGCCCTTA-----CCCATGGGGTGGGTACAGGCCGCCCAAGACAG 102
Qy 23 AlaHisLeuLysProSerGlnLeuSerSerPheSer---TrpAspAsnCysPheGlu 41
Db 103 GCCGTATCAGGAGGCCCTTCTCTCAGGGGCTGCCCTCTGGGATAAC-----153
Qy 42 GlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValValPro 61
Db 154 -----CACCCCGCCCTTCTCTGGGTTTCCT 177
Qy 62 GlyAsnValThrLeuSerValValGlySerThrSerVal-----74
Db 178 GTTTCCTAT---CTGGCTGCAGTTTCTCAGTCCCTTGTGGATTTCCTCCATGGTCTGTCC 234
Qy 75 ProLeuSerProLeuLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrp 94
Db 235 CCATCATACCTCTCTCGCAAAACCTTGCTACTG-----GGCTGCAC 279
Qy 95 IleLysIleProCysThrAspTyrIleGlySerCysThrPheGluHisPheCysAspVal 114
Db 280 CTGGCAAAATCCATGCTCAGCACAGCGGGATCAAGACCTCTCAATACAACTGT-----333
Qy 115 LeuAspMetLeuIleProThrGlyLupProCysProGluProLeuArgThrTyrGlyLeu 134
Db 334 -----CTCTGCCAAT-----CCCTGCCCGCAGCGCTGAGCCCGCCAGTCTGAAA 377
Qy 135 ProCysHisCys---ProPheLysGlu-GlyThrTyrSerLeuProLysSerGluPheAl 153
Db 378 CCAGGGAGTGTCTCTCTTCTCTCCCTTGACCTCACCTCAGACCATGCCAAATCTG 437
Qy 153 aValProAspLeu-----GluLeuProSerTrpLeuThrThrGlyAs 167
Db 438 CCTCTAAACCTCCAGCCAGCCCTCCCGCAGCTCCAGTGACAGTGTCTCAGGTAC 497
Qy 167 nTyrArgIleGluSerValLeu 174
Db 498 CTGAGCTCAGCTCTCGGTGCTA 519

RESULT 11
; Sequence 78, Application US/09168595
; Patent No. 6555866
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Transcripts Encoding Immunomodulatory
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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Db 438 CCTCTAAACCTCCAGGAGGAGGCTCCCGAGCTCCAGTGCAGTGTCTCAGGTAC 497
QY 167 nTyrArgIleGluSerValLeu 174
Db 498 CTGAGCTCAGCTCTCGGTGCTA 519
RESULT 12
US-07-866-979-5/c
; Sequence 5, Application US/07866979
; Patent No. 5532347
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Mountjoy, Kathleen G
; TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/866,979
; FILING DATE: 19920410
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532347nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 462..1415
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..461
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1416..1633
US-07-866-979-5
Alignment Scores:
Pred. No.: 1.07 Length: 1633
Score: 89.50 Matches: 49
Percent Similarity: 38.25% Conservative: 21
Best Local Similarity: 26.78% Mismatches: 62
Query Match: 8.79% Indels: 51
DB: 1 Gaps: 8
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QY 34 PheSerTrpAspAnCys-----PheGluGlyLysAspProAlaValIleArgSerLeu 51

Db 535 CCCAGCTGGGGATGGCTGTGGGGGTGGAGTTGAGGGAGCCC-----AGAGTCTT 485
QY 52 ThrLeuGluProAspProIleValValProGlyAsnValThrLeuSerValValGlySer 71
Db 484 CTCCTGGATCCCTGCACAGCCATAGTCTGTCCAGGAAGCAGGAGGATCGTTGGAGGC 425
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QY 112 CysAspValLeuAspMet-LeuIleProThrGlyGluPro-----CysPro--GluPro 128
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QY 146 -----SerLeuProLysSerGluPheAlaValProAspLeuGlu 158
Db 238 CAACCGCTGGGCTCAGGATTTCTCAACACGAGCTGTCTCAGTCCCTCCCTGCT 179
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QY 178 Y 178
Db 118 C 118
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; Sequence 5, Application US/08466906B
; Patent No. 5849871
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Mountjoy, Kathleen G
; TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,906B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5849871nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,154-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..461
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 462..1415
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1416..1633
; US-08-466-906B-5

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Score: 89.50 Matches: 49
Percent Similarity: 38.25% Conservative: 21
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Query Match: 8.79% Indels: 51
DB: 2 Gaps: 8

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Qy 52 ThrLeuGluProAspProIleValValProGlyAsnValThrLeuSerValValGlySer 71
Db 484 CTCTGGATCCCTGCACAGCATAGTCTCTCCAGGAGCAGGAGAGCGTGGTGGAGGC 425
Qy 72 ThrSerValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAla 91
Db 424 CTCAGGTCCCGACAGATTCCTCCCTCCAGGTGCTCTGCTTAGTTCATGTTGCTGCCAGG 365
Qy 92 GlyLeuTrpIleLysIleProCysThrAspTyrIleGlySerCysThrPheGluHisPhe 111
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Qy 112 CysAspValLeuAspMet-LeuIleProThrGlyGluPro-----CysPro--GluPro 128
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Qy 146 -----SerLeuProLysSerGluPheAlaValProAspLeuGlu 158
Db 238 CAACCGCTGGGCTCAGGGATTCTCACAAACAGCGCTGGTCTCTCAGCTCCCTCCCTGCCT 179
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Db 178 CTTCCCTGGGTGGTGTGCTCAGGTCCAGGACATTCGACACCTCTGGACCGTCTGTGG 119
Qy 178 Y 178
Db 118 C 118

RESULT 14
US-08-706-281A-5/c
; Sequence 5, Application US/08706281A
; Patent No. 6100048
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Fan, Wei
; APPLICANT: Boston, Bruce A
; APPLICANT: Kesterton, Robert A
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; APPLICANT: Lu, Dongsei
; APPLICANT: Chen, Wenbiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagonists
; TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,281A
; FILING DATE: 04-SRP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6100048nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..461
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 462..1415
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1416..1633
; US-08-706-281A-5

Alignment Scores:
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Score: 89.50 Matches: 49
Percent Similarity: 38.25% Conservative: 21
Best Local Similarity: 26.78% Mismatches: 62
Query Match: 8.79% Indels: 51
DB: 3 Gaps: 8

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Qy 52 ThrLeuGluProAspProIleValValProGlyAsnValThrLeuSerValValGlySer 71
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Qy 72 ThrSerValProLeuSerSerProLeuLysValAspLeuValLeuGluLysGluValAla 91
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QY 92 GlyLeuTrpIleLysLeuProCysThrAspTyrIleGlySerCysThrPheGluHisPhe 111
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QY 146 -----SerLeuProLysSerGluPheAlaValProAspLeuGlu 158
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; Sequence 5, Application US/09201746
; Patent No. 6268221
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Mountjoy, Kathleen G
; TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
; TITLE OF INVENTION: and Uses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 01-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6268221nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,154-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..461
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 462..1415
; FEATURE:

; NAME/KEY: 3'UTR
; LOCATION: 1416..1633
; US-09-201-746-5

Alignment Scores:

Pred. No.: 1 07 Length: 1633
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Percent Similarity: 38.25% Conservative: 21
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1005	98.7	2436	10	US-09-525-978B-81	Sequence 81, Appl
3	1005	98.7	2436	21	US-10-843-641A-1447	Sequence 1447, Ap
4	1005	98.7	2478	17	US-10-170-385-390	Sequence 390, App
5	1000	98.2	953	20	US-10-723-860-528	Sequence 528, App
6	1000	98.2	1935	10	US-09-971-352-102	Sequence 102, App
7	1000	98.2	2384	9	US-09-822-849A-53	Sequence 53, Appl
8	1000	98.2	3988	20	US-10-723-860-5187	Sequence 5187, Ap
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c 25	254	25.0	857	13	US-10-027-632-164063	Sequence 164063,
c 26	254	25.0	857	13	US-10-027-632-164064	Sequence 164064,
c 27	254	25.0	857	13	US-10-027-632-164065	Sequence 164065,
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c 32	145	14.2	593	13	US-10-027-632-277778	Sequence 277778,
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38	97.5	9.6	20966	9	US-09-909-547-7	Sequence 7, Appl
39	97.5	9.6	20966	15	US-10-231-814-7	Sequence 7, Appl
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44	95.5	9.4	638	21	US-10-487-901-3700	Sequence 3700, Ap
45	95.5	9.4	670	21	US-10-487-901-3699	Sequence 3699, Ap

ALIGNMENTS

RESULT 1
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; Sequence 380, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; FILE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034

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; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 380
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-380

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Score: 1005.00 Matches: 191
Percent Similarity: 98.96% Conservative: 0
Best Local Similarity: 98.96% Mismatches: 2
Query Match: 98.72% Indels: 0
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US-10-030-937-9 (1-193) x US-09-954-531-380 (1-2436)

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Db 299 AAGGTGGATTAGTTTGGAGAAGAGGTGGCTCTCGATCAAGATCCCATGCACA 358
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Qy 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuLeuPro 120
|||
Db 359 GACTACATTGGCAGCTGACTTGAACACTTCTGTGATGTCTTGACATGTTAATTCCT 418
|||
Qy 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
|||
Db 419 ACTGGGAGCCCTGCCAGAGCCCTCGTACCTATGGGCTTCTTGCCACTGTCCCTTC 478
|||
Qy 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 160
|||
Db 479 AAAGAAGGAACCTACTCAGTCCCAAGAGGAATTCGTTGTGCTGACCTGGAGCTGCC 538
|||
Qy 161 SerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysArg 180
|||
Db 539 AGTTGGCTCACCACCGGAAGTACCGCATAGAGAGCTCTGAGCAGCACTGGGAGCGT 598
|||
Qy 181 LeuGlyCysLysLysIleAlaAlaSerLeuLysGlyIle 193
|||
Db 599 CTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGCATA 637
|||

RESULT 2

US-09-525-978B-81
; Sequence 81, Application US/09525978B
; Publication No. US2003004972A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Caras, Ingrid W.
; APPLICANT: Hevezl, Peter
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING MACROPHAGE DEVELOPMENT

;
; TITLE OF INVENTION: RELATED DISORDERS, COMPOSITIONS, AND METHODS OF
; FILE OF INVENTION: SCREENING FOR MACROPHAGE DEVELOPMENT MODULATORS
; FILE REFERENCE: A-67413-1/DJB/JJD
; CURRENT APPLICATION NUMBER: US/09/525,978B
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: USSN 60/124,530
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-978B-81

Alignment Scores:
Pred. No.: 6.47e-117 Length: 2436
Score: 1005.00 Matches: 191
Percent Similarity: 98.96% Conservative: 0
Best Local Similarity: 98.96% Mismatches: 2
Query Match: 98.72% Indels: 0
DB: 10 Gaps: 0

US-10-030-937-9 (1-193) x US-09-525-978B-81 (1-2436)

Qy 1 MetGlnSerLeuMetGlnAlaProLeuLeuLeuLeuLeuLeuLeuAlaThrPro 20
|||
Db 59 ATGCAGTCCCTGATGCAGGCTCCCTCTGATCGCCCTGGCTTGTCTTCGGGACCCCT 118
|||
Qy 21 AlaGlnAlaHisLeuLysProSerGlnLeuSerSerPheSerTrpAspAnCysPhe 40
|||
Db 119 GCGCAAGCCACCTGAAAAAGCCATCCAGCTCAGTAGCTTTTCTCTGGGATACTGTGAT 178
|||
Qy 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
|||
Db 179 GAAGGGAAGACCTCGCGGTGATCAGAAGCTGACTCTGAGGCTGACCCCATCGTCGT 238
|||
Qy 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
|||
Db 239 CCTGGAATGTGACCTCAGTGTGCTGGCAGCACCACTGTCCTCCCTGAGTCTCTCTCTG 298
|||
Qy 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuThrLysLysLysProCysThr 100
|||
Db 299 AAGGTGGATTAGTTTGGAGAAGAGGTGGCTCTCGATCAAGATCCCATGCACA 358
|||
Qy 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuLeuPro 120
|||
Db 359 GACTACATTGGCAGCTGACTTGAACACTTCTGTGATGTCTTGACATGTTAATTCCT 418
|||
Qy 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
|||
Db 419 ACTGGGAGCCCTGCCAGAGCCCTCGTACCTATGGGCTTCTTGCCACTGTCCCTTC 478
|||
Qy 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 160
|||
Db 479 AAAGAAGGAACCTACTCAGTCCCAAGAGGAATTCGTTGTGCTGACCTGGAGCTGCC 538
|||
Qy 161 SerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysArg 180
|||
Db 539 AGTTGGCTCACCACCGGAAGTACCGCATAGAGAGCTCTGAGCAGCACTGGGAGCGT 598
|||
Qy 181 LeuGlyCysLysLysIleAlaAlaSerLeuLysGlyIle 193
|||
Db 599 CTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGCATA 637
|||

RESULT 3

US-10-843-641A-1447
; Sequence 1447, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; Signature Gene Sets

```
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1447
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-1447

Alignment Scores:
Pred. No.: 6,47e-117 Length: 2436
Score: 1005.00 Matches: 191
Percent Similarity: 98.96% Conservative: 0
Best Local Similarity: 98.96% Mismatches: 2
Query Match: 98.72% Indels: 0
DB: 21 Gaps: 0

US-10-030-937-9 (1-193) x US-10-843-641A-1447 (1-2436)

QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuAlaLeuGlyLeuLeuLeuAlaThrPro 20
DB 59 ATGCAGTCCCTGATGCAGGCTCCCTCTGATGCCCTGGGCTTGTCTTCGCGACCCCT 118
QY 21 AlaGlnAlaHisLeuLeuLeuProSerGlnLeuSerSerPheSerTrpAspLeuPhe 40
DB 119 GCGCAAGCCCACTGAAAGCCATCCAGCTCAGTAGCTTTTCTCGGATACCTGTGAT 178
QY 41 GluGlyLeuAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
DB 179 GAAGGGAAGGACCTCGCGGTGATCAGAAGCCTGACCTGGAGCCTGACCCCATCGTGT 238
QY 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
DB 239 CCTGGAATGTGACCTCAGTCTGCTGGGAGCAGCAGTGTCCCTGAGTTCTCTCTG 298
QY 81 LysValAspLeuValLeuGluLeuValAlaGlyLeuTrpIleLeuProCysThr 100
DB 299 AAGGTGATTTAGTTTGGAGAGGAGGTGGCTGGCCCTCGGATCAAGATCCCATGCACA 358
QY 101 AspTyrlleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuLeuPro 120
DB 359 GACTACATTGGCAGCTGACCTTTGAACACTTCTGTGATGTGTTGACATGTTAATCTCT 418
QY 121 ThrGlyGluProCysProGluProLeuArgThrTyrlleGlyLeuProCysHisCysProPhe 140
DB 419 ACTGGGAGCCCTGCCAGAGCCCTCGCTGCTACCTATATGGGCTTCTTGGCCACTGTCTC 478
QY 141 LysGluGlyThrTyrlleSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 160
DB 479 AAAGAAGGAACCTACTCACTGCCCCCAAGAGCGAATTCGTTGTGCTTACCTGGAGCTGCC 538

; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1447
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-1447

Alignment Scores:
Pred. No.: 6,47e-117 Length: 2436
Score: 1005.00 Matches: 191
Percent Similarity: 98.96% Conservative: 0
Best Local Similarity: 98.96% Mismatches: 2
Query Match: 98.72% Indels: 0
DB: 21 Gaps: 0

US-10-030-937-9 (1-193) x US-10-170-385-390 (1-2478)

QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuAlaLeuGlyLeuLeuLeuAlaThrPro 20
DB 96 ATGCAGTCCCTGATGCAGGCTCCCTCTGATGCCCTGGGCTTGTCTTCGCGACCCCT 155
QY 21 AlaGlnAlaHisLeuLeuLeuProSerGlnLeuSerSerPheSerTrpAspLeuPhe 40
DB 156 GCGCAAGCCCACTGAAAGCCATCCAGCTCAGTAGCTTTTCTCGGATACCTGTGAT 215
QY 41 GluGlyLeuAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
DB 216 GAAGGGAAGGACCTCGCGGTGATCAGAAGCCTGAGCTCGGAGCCTGACCCCATCGTGT 275
QY 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
DB 276 CTGGAATGTGACCTCAGTGTCTGGGAGCAGCAGTGTCCCTGAGTTCTCTCTG 335
QY 81 LysValAspLeuValLeuGluLeuValAlaGlyLeuTrpIleLeuProCysThr 100
DB 336 AAGGTGATTTAGTTTGGAGAGGAGGTGGCTGGCCCTCGGATCAAGATCCCATGCACA 395
QY 101 AspTyrlleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuLeuPro 120
DB 396 GACTACATTGGCAGCTGACCTTTGAACACTTCTGTGATGTGCTTACCTGAGTTAATCTCT 455
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QY 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
Db 456 ACTGGGAGGAGCCCTGCCAGAGCCCTCGTACCTATGGGTTCTCTGCCACTGTCCTCCCTTC 515
QY 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 160
Db 516 AAAGAAGAACCTACTCACTGCCCAAGAGCGAATTCTGTGCTGACCTGGAGCTGCC 575
QY 161 SerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysArg 180
Db 576 AGTTGGCTCACCCAGCGGAACCTACCGCATAGAGAGCGTCTGAGCAGCAGTGGGAAGCGT 635
QY 181 LeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
Db 636 CTGGGCTGCATCAAGATCGCTGCCCTCTCTAAAGGGCATA 674

RESULT 5
US-10-723-860-528
; Sequence 528, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 528
; LENGTH: 953
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-528

Alignment Scores:
Pred. No.: 7,3e-117 Length: 953
Score: 1000.00 Matches: 190
Percent Similarity: 98.45% Conservative: 0
Best Local Similarity: 98.45% Mismatches: 3
Query Match: 98.23% Indels: 0
DB: 20 Gaps: 0

US-10-030-937-9 (1-193) x US-10-723-860-528 (1-953)
QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
Db 91 ATGCAGTCCCTGTATGCAGGCTCCCTCTGATGCCCTGGGCTTGTCTCGGGGCCCT 150
QY 21 AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db 151 GCGCAAGCCCACTGAAAAGCCATCCAGCTCAGTAGCTTTCCTGGGTAATCTGTGAT 210
QY 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
Db 211 GAAGGAAGGACCCCTGGGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATCGTCGTT 270
QY 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
Db 271 CCTGGAATGTGACCCCTCAGTGTCTGGGAGCAGCACCAGTGTCCCTCAGTTCCTCTG 330
QY 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
Db 331 AAGTGGATTAGTTTGGAGAAGAGGTGCTGCTCTGTCGATCAAGATCCCATGCACA 390
QY 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
Db 391 GACTACATTGGCAGCTGTACCTTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCCT 450
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```
QY 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
Db 451 ACTGGGAGGAGCCCTGCCAGAGCCCTCGTACCTATGGGTTCTCTGCCACTGTCCTCCCTTC 510
QY 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 160
Db 511 AAAGAAGAACCTACTCACTGCCCAAGAGCGAATTCTGTGCTGACCTGGAGCTGCC 570
QY 161 SerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysArg 180
Db 571 AGTTGGCTCACCCAGCGGAACCTACCGCATAGAGAGCGTCTGAGCAGCAGTGGGAAGCGT 630
QY 181 LeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
Db 631 CTGGGCTGCATCAAGATCGCTGCCCTCTCTAAAGGGCATA 669

RESULT 6
US-09-971-392-102
; Sequence 102, Application US/09971392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, David P.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Pearson, Cecelia I.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 102
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Template ID: 977615.8
US-09-971-392-102

Alignment Scores:
Pred. No.: 2,02e-116 Length: 1935
Score: 1000.00 Matches: 190
Percent Similarity: 98.45% Conservative: 0
Best Local Similarity: 98.45% Mismatches: 3
Query Match: 98.23% Indels: 0
DB: 10 Gaps: 0

US-10-030-937-9 (1-193) x US-09-971-392-102 (1-1935)
QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
Db 102 ATGCAGTCCCTGTATGCAGGCTCCCTCTGATGCCCTGGGCTTGTCTCGGGGCCCT 161
QY 21 AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db 162 GCGCAAGCCCACTGAAAAGCCATCCAGCTCAGTAGCTTTCCTGGGTAATCTGTGAT 221
QY 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
Db 222 GAAGGAAGGACCCCTGGGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATCGTCGTT 281
QY 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
Db 282 CCTGGAATGTGACCCCTCAGTGTCTGGGAGCAGCACCAGTGTCCCTCAGTTCCTCTG 341
QY 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
Db 342 AAGTGGATTAGTTTGGAGAAGAGGTGCTGCTCTGTCGATCAAGATCCCATGCACA 401
QY 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
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Db 402 GACTACATTGGGAGCTGTACCTTTGAACACTTCTGTGATGTGCTTACATGTTAATTCCT 461
QY 121 ThrGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
Db 462 ACTGGGGGCCCTGCCAGAGCCCTCGGTACCTATGGGCTTCTTGCCACCTGTCCTTC 521
QY 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 160
Db 522 AAAGAAGGAACCTACTCACTGCCCAAGAGCGAATTCGTTGTGCTGACCTGGAGCTGCC 581
QY 161 SerTrpLeuThrThrGlyAsnTyrArgGileGluSerValLeuSerSerGlyLysArg 180
Db 582 AGTTGGCTCACCACCGGGAACCTACCCATAGAGAGCGTCTTGAGCAGCAGTGGAGCGT 641
QY 181 LeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
Db 642 CTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGCATA 680

RESULT 7

US-09-822-849A-53
; Sequence 53, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-53

Alignment Scores:
Pred. No.: 2,72e-116 Length: 2384
Score: 1000.00 Matches: 190
Percent Similarity: 98.45% Conservative: 0
Best Local Similarity: 98.45% Mismatches: 3
Query Match: 98.23% Indels: 0
DB: 9 Gaps: 0

US-10-030-937-9 (1-193) x US-09-822-849A-53 (1-2384)

QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
Db 13 ATGCATCTCCTGATGAGGCTCCCTTCCCTGATGCGCCCTGGGCTTGCTTCTGGGGCCCT 72
QY 21 AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db 73 GGCAGAGCCACCTGAAAAGCCATCCAGCTCAGTAGCTTTTCTCGGATTAACGTGTAT 132
QY 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
Db 133 GAAGGGAAGGACCCCTCGGTGATCAGAAGCTGACCTGAGGCTGACCCCACTCGTCGT 192
QY 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
Db 193 CCTGGGAATGTGACCTCAGTGTGTGGGAGCAGCAGGTGTCCTCCCTGAGTTCTCTCTG 252

QY 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
Db 253 AAGGTGGATTTAGTATTTTGGAGAAGGAGGTGGCTGCCCTCTGGATCAAGATCCCATGCACA 312
QY 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
Db 313 GACTACATGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCCT 372
QY 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
Db 373 ACTGGGGAGCCCTGCCAGAGCCCTGGGTACTATGGGCTTCTTGCCACCTGTCCTTC 432
QY 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro 160
Db 433 AAAGAAGGAACCTACTCACTGCCCAAGAGCGAATTCGTTGTGCTGACCTGGAGCTGCC 492
QY 161 SerTrpLeuThrThrGlyAsnTyrArgGileGluSerValLeuSerSerGlyLysArg 180
Db 493 AGTTGGCTCACCACCGGGAACCTACCCATAGAGAGCGTCTTGAGCAGCAGTGGAGCGT 552
QY 181 LeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
Db 553 CTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGCATA 591

RESULT 8

US-10-723-860-5187
; Sequence 5187, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natacha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5187
; LENGTH: 3988
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2864)..(2894)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3472)..(3486)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-5187

Alignment Scores:
Pred. No.: 5.69e-116 Length: 3988
Score: 1000.00 Matches: 190
Percent Similarity: 98.45% Conservative: 0
Best Local Similarity: 98.45% Mismatches: 3
Query Match: 98.23% Indels: 0
DB: 20 Gaps: 0

US-10-030-937-9 (1-193) x US-10-723-860-5187 (1-3988)

QY 1 MetGlnSerLeuMetGlnAlaProLeuLeuIleAlaLeuGlyLeuLeuAlaThrPro 20
Db 96 ATGCATCTCCTGATGAGGCTCCCTTCCCTGATGCGCCCTGGGCTTGCTTCTCGGGCCCT 155
QY 21 AlaGlnAlaHisLeuLysLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe 40
Db 156 GGCAGAGCCACCTGAAAAGCCATCCAGCTCAGTAGCTTTTCTCGGATTAACGTGTAT 215

Qy	41	GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal	60
Db	216	GAAGGGAAGGACCCCTCGCGTGCATCAGAAAGCCTGACTCTGGAGCGCTGACCCCATCGTCGT	275
Qy	61	ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu	80
Db	276	CTTGGAAATGTGACCCCTCAGTGTGCTGGCAGCACCAGTGTCCCCCTGAGTCTCTCTCTG	335
Qy	81	LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr	100
Db	336	AAAGTGGATTTAGTTTTCGAGAAGAGGTGCTGGCCTCTGGATCAAGATCCCATGCACA	395
Qy	101	AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro	120
Db	396	GACTACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTCTGTGATGTTAAATTCCT	455
Qy	121	ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe	140
Db	456	ACTGGGGAGCCCTGCCAGAGCCCTCGGTACCTATGGGCTTCCTTCCCACTGTGCCCTTC	515
Qy	141	LysGluGlyThrTyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuPro	160
Db	516	AAAGAAGGAACCTACTCTCATGCTCCCAAGAGCGAAATTCGTTGTGCCCTGACCTGGAGCTGCC	575
Qy	161	SerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysArg	180
Db	576	AGTTGGCTCACCACCGGGNACTACCGCATAGAGAGCGTCTTGACGACAGTGGGAAGCGT	635
Qy	181	LeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle	193
Db	636	CTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGGCATA	674

RESULT 9

```

US-10-388-934-167
; Sequence 167, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
; APPLICANT: Boess, Franziska
; APPLICANT: Suter-Dick, Laura
; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 1983
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-388-934-167

```

[illegible]

```

RESULT 11
US-10-972-079-7219
; Sequence 7219, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7219
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Chicken 19866894191999_2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(32)
; OTHER INFORMATION: n is any nucleotide
US-10-972-079-7219

```

```

Alignment Scores:
Pred. No.:      1.42e-36      Length:      596
Score:          367.50      Matches:      70

```

Percent Similarity:	62.84%	Conservative:	23
Best Local Similarity:	47.30%	Mismatches:	30
Query Match:	36.10%	Indels:	26
DB:	22	Gaps:	2

US-10-030-937-9 (1-193) x US-10-972-079-7219 (1-596)

Qy	69	ValGlySerThrSerValProLeuSerSerPro---	LeuLysValAspLeuValLeuGlu	87
		:::	:::	
Db	51	GTCGGAGGGAGGGCTGGGTGCAGCGTCTCTT	CACAGCGGTGCTGGTGGGAG	110
		:::	:::	
Qy	88	LysGluValAlaGlyLeuTrpIleLysIleProCys	ThrAspTyIleGlySerCysThr	107
		:::	:::	
Db	111	AAGCCTTGGGTGACCTTGATCCAGCTGCCTGC	ATCGACAGCTGGCAGCTGCAC	170
		:::	:::	
Qy	108	PheGluHisPheCysAspValLeuAspMetLeuIle	ProThrGlyGluProCysProGlu	127
		:::	:::	
Db	171	TATGATGATGTGTCAACATCTCGACAACTCAT	CCACCGGCACRCCCTGCCGGAG	230
		:::	:::	
Qy	128	ProLeuArgThrTyrglyLeuProCysHisCysP	roPheLysGluGlyThr----	144
		:::	:::	
Db	231	CCGCTGTCACTACGGGATCCCTGCCACTGCCCT	TCAAGGC--GGTACGTCCCAACAC	289
		:::	:::	
Qy	144	-----	-----	144
		:::	:::	
Db	290	CGGCTGCCCTYGGTGCTGTGGGTGGTGTGGCT	CACGACGCCCTCTCTCTGCAGGGC	349
		:::	:::	
Qy	145	---TyrSerLeuProLysSerGluPheAlaValP	roAspLeuGluLeuProSerTrpLeu	163
		:::	:::	
Db	350	TCCTACTCACTGCCCGCAGCGACTTGGCCCTG	CCCGACGTGAGCTGCCCTCCTGGATG	409
		:::	:::	
Qy	164	ThrThrGlyAenTyraGileGluSerValLeuSer	SerGlyLysArgLeuGlyCys	183
		:::	:::	
Db	410	ACCAACGGCAACTACCTGTGCGAGTGGTCTG	TCAGCAACAAGGGCAGAGCTCGCTCG	469
		:::	:::	
Qy	184	IleLysIleAlaAlaSerLeuLys	191	
		:::	:::	
Db	470	GTCAAGCTGGGCTTCTCTTTCGAC	493	
		:::	:::	

RESULT 12

```

US-10-972-079-7218
; Sequence 7218, Application US/10972079
; Publication No. US2005015317A1
;
; GENERAL INFORMATION:
;
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
;
; TITLE OF INVENTION: METHODS & SYSTEMS FOR
; TITLE OF INVENTION: LIVESTOCK
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079,
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 7218
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Chicken 19866894191999_1
; FEATURE:
;
; NAME/KEY: misc_feature
; LOCATION: (1)..(114)
; OTHER INFORMATION: n is any nucleotide
US-10-972-079-7218

```

Alignment Scores:	
Pred. No.:	1.43e-36
Score:	367.50
Percent Similarity:	62.84%
Length:	599
Matches:	70
Conservative:	23

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Best Local Similarity: 47.30% Mismatches: 30
Query Match: 36.10% Indels: 26
DB: 22 Gaps: 2

US-10-030-937-9 (1-193) x US-10-972-079-7218 (1-599)
Qy 69 ValGlySerThrSerValProLeuSerSerPro---LeuLysValAspLeuValLeuGlu 87
    |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 133 GTCGGAGGGAGGGCTGGGTGCTCAGTGTCCCTTTCACAGCGGTGCTGGTGGAG 192

Qy 88 LysGluValAlaGlyLeuTrpLleLysIleProCysThrAspTyrIleGlySerCysThr 107
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 193 AAGCCCTTGGGTGACCTCTCGATCCAGCTGCCCTGCATCCAGCAGCTGGCAGCTGCACC 252

Qy 108 PheGluHisPheCysAspValLeuAspMetLeuIleProThrGlyGluProCysProGlu 127
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 253 TAGATGATGTGCAACATCTTCGACAACTATCCACCAGCGACRCCCTGCCCGAG 312

Qy 128 ProLeuArgThrTyrGlyLeuProCysHisCysProPheLysGluGlyThr----- 144
    |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 313 CCGCTGTCTACCTAGCGCATCCCTGCCACTGCCCTTCAAGGC-GGTACGTCCCAAC 371

Qy 144 ----- 144
Db 372 CGCGTGCCTTGGTGTGGGTGGGTGGTGTGGCTCAGCAGGCCCTCTCTCGAGGGC 431

Qy 145 ---TyrSerLeuProLysSerGluPheAlaValProAspLeuGluLeuProSerTrpLeu 163
    |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 432 TCCTACTACTGCCCGCAGGACTTGCCTTGCCTGCCAGCTGAGCTGCCCTCTCGATG 491

Qy 164 ThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysArgLeuGlyCys 183
    |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 492 ACCAAGCGCACTACCGTGTGCGAGTGTGTGTCAGCAACAAGGGCGAGGAGCTCGCCTGC 551

Qy 184 IleLysIleAlaLalaSerLeuLys 191
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 552 GTCAAGCTGGGCTTCTCTCTTGCAG 575

RESULT 13
US-09-864-761-1518/c
; Sequence 1518, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1518
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011342.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
US-09-864-761-1518

Alignment Scores:
Pred. No.: 5,38e-35 Length: 475
Score: 354.00 Matches: 61
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.39% Mismatches: 0
Query Match: 34.77% Indels: 0
DB: 9 Gaps: 0

US-10-030-937-9 (1-193) x US-09-864-761-1518 (1-475)
Qy 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpLleLysIleProCysThr 100
    :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 468 CAGGTGGATTTAGTTTGGAGAGGAGGTGGCTCTGGATCAAGATCCCATGCACA 409

Qy 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
    |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 408 GACTACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCCT 349

Qy 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
    |||||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 348 ACTGGGGAGCCCTGCCAGAGCCCTGCGTACCTATGGGCTTCTTGGCCACTGTCCTTC 289

Qy 141 LysGlu 142
    |||||
Db 288 AAAGAA 283

RESULT 14
US-09-969-034-4215
; Sequence 4215, Application US/09969034
; Publication No. US20040110688A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Astle, Jon H.
; APPLICANT: Carroll, Eddie III
; APPLICANT: Catino, Theodore J.
; APPLICANT: Dwivedi, Poornima
; APPLICANT: Molino, Gary A.
; APPLICANT: Thiagalingam, Arunthathi
```

```
; APPLICANT: Lewis, Marcia E.
; TITLE OF INVENTION: Nucleic Acid Sequences Differentially
; FILE REFERENCE: 1657/1032
; CURRENT APPLICATION NUMBER: US/09/969,034
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/237,271
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 4494
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4215
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 241, 277, 288, 295, 299, 300, 304, 310, 316, 343, 346, 356,
; LOCATION: 364, 370, 396, 397, 406, 410, 415, 424, 437
; OTHER INFORMATION: n = A,T,C or G
US-09-969-034-4215

Alignment Scores:
Pred. No.: 2,34e-32 Length: 448
Score: 333.00 Matches: 62
Percent Similarity: 98.41% Conservative: 0
Best Local Similarity: 98.41% Mismatches: 1
Query Match: 32.71% Indels: 0
DB: 11 Gaps: 0

US-10-030-937-9 (1-193) x US-09-969-034-4215 (1-448)

QY 131 ThrTyrGlyLeuProCysHisCysProPheLysGluGlyThrTyrSerLeuProLysSer 150
Db 1 ACCTATGGGCTTCCTGCGCACTGCTCCCTTCAAAGAAGGAACCTACTCACTGCCCAAGAGC 60
QY 151 GluPheAlaValProAspLeuGluLeuProSerTyrLeuThrThrGlyAsnTyrArgIle 170
Db 61 GAATTCTGTGTGCTGACCTGAGCTGGAGCTGCCAGTTGGCTCACCACCGGAACCTACCGCAT 120
QY 171 GluSerValLeuSerSerGlyLysArgLeuGlyCysIleLysIleAlaAlaSerLeu 190
Db 121 GAGAGCGTCTTGAGCAGCAGTGGGAGAGCGTCTGGGCTGCATCAAGATCGCTGCTCTCTA 180
QY 191 LysGlyIle 193
Db 181 AAGGGCATA 189

RESULT 15
US-10-027-632-207798
; Sequence 207798, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207798
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207798

Alignment Scores:
Pred. No.: 1.84e-24 Length: 546
Score: 272.00 Matches: 57
Percent Similarity: 86.76% Conservative: 2
Best Local Similarity: 83.82% Mismatches: 7
Query Match: 26.72% Indels: 2
DB: 13 Gaps: 1

US-10-030-937-9 (1-193) x US-10-027-632-207798 (1-546)

QY 27 LysProSerGlnLeuSerSerPheSerTyrAspAsnCysPheGluGlyLysAspProAla 46
Db 255 CAGCCATCCCACTCAGTAGCTTTTCTGGGATAACTGTGATGAAGGAAGGACCTCGG 314
QY 47 ValIleArgSerLeuThrLeuGluProAspProIleValValProGlyAsnValThrLeu 66
Db 315 GTGATCAGAAGCTGACTCTGGAGCTGACCCCATCTCGTTCCTGGAAATGTGACCTC 374
QY 67 SerValValGlySerThrSerValProLeuSerSerProLeuLysValAspLeuValLeu 86
Db 375 AGTGTCTRTGGGCAGCACCAGTGTCCCTCTGAGTTCCTCTCTGAGGTGAGCCTGGGGTG 434
QY 87 -----GluLysGluValAlaGly 92
Db 435 GGTGGAGAAGGGGAGGTGCGAGGG 458

Search completed: July 27, 2005, 22:48:00
Job time : 1193.74 secs
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OM protein - protein search, using sw model

Run on: July 27, 2005, 18:58:36 ; Search time 36.8844 Seconds
(without alignments)
390.606 Million cell updates/sec

Title: US-10-030-937-9
Perfect score: 193
Sequence: 1 MOSLMOAPLILALLLATT.....LSSSGKRLGCIKIAASLKI 193

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/iaa/6B COMB pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	58.0	178	4	US-09-183-841-2
2	112	58.0	183	4	US-09-183-841-1
3	10	5.2	362	4	US-09-902-540-12082
4	9	4.7	262	3	US-08-961-083-98
5	9	4.7	262	4	US-09-536-784-98
6	9	4.7	270	3	US-08-961-083-206
7	9	4.7	270	4	US-09-536-784-206
8	9	4.7	231	4	US-09-583-110-4201
9	9	4.7	328	4	US-09-107-433-3318
10	8	4.1	390	4	US-09-949-016-6952
11	8	4.1	444	4	US-09-252-991A-20496
12	8	4.1	563	4	US-09-252-991A-23790
13	8	4.1	769	3	US-09-320-878-12
14	8	4.1	769	4	US-09-141-908-10
15	8	4.1	769	4	US-09-657-440-12
16	8	4.1	809	3	US-09-105-537-24
17	8	4.1	3782	3	US-09-105-537-4
18	7	3.6	85	4	US-09-270-767-32129
19	7	3.6	85	4	US-09-270-767-47346
20	7	3.6	96	3	US-08-936-165A-401
21	7	3.6	103	4	US-09-270-767-33345
22	7	3.6	103	4	US-09-270-767-48562
23	7	3.6	115	4	US-09-746-801A-47
24	7	3.6	153	3	US-09-199-637A-213
25	7	3.6	168	4	US-09-902-540-16420
26	7	3.6	170	4	US-09-205-258-1011
27	7	3.6	213	4	US-09-902-540-13301

28 7 3.6 267 4 US-09-489-039A-12889 Sequence 12889, A
29 7 3.6 269 4 US-09-543-681A-6475 Sequence 6475, Ap
30 7 3.6 285 1 US-08-149-803-24 Sequence 24, Appl
31 7 3.6 287 4 US-09-540-236-2879 Sequence 2879, Ap
32 7 3.6 301 4 US-09-902-540-11985 Sequence 11985, A
33 7 3.6 315 4 US-09-252-991A-31850 Sequence 31850, A
34 7 3.6 324 4 US-09-489-039A-7803 Sequence 7803, Ap
35 7 3.6 325 2 US-08-828-242-4 Sequence 4, Appl
36 7 3.6 325 3 US-09-206-499-4 Sequence 3, Appl
37 7 3.6 331 2 US-08-828-242-3 Sequence 5, Appl
38 7 3.6 331 3 US-08-910-927B-5 Sequence 3, Appl
39 7 3.6 331 3 US-09-206-499-3 Sequence 5, Appl
40 7 3.6 331 3 US-09-270-270-5 Sequence 11, Appl
41 7 3.6 331 4 US-09-961-403-11 Sequence 9513, Ap
42 7 3.6 348 4 US-09-949-016-9513 Sequence 5, Appl
43 7 3.6 355 4 US-09-580-929-5 Sequence 1008, Ap
44 7 3.6 364 4 US-09-205-258-1008 Sequence 8053, Ap
45 7 3.6 369 4 US-09-489-039A-8053

ALIGNMENTS

RESULT 1
US-09-183-841-2
; Sequence 2, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: His tag at residues 1 to 17
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence of GM2 protein using His6 tag
US-09-183-841-2

Query Match 58.0%; Score 112; DB 4; Length 178;
Best Local Similarity 100.0%; Pred. No. 3.1e-102;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 EGKDPVIRSLTLEPDPPIVPGNVTLSVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCT 100
Db 26 EGKDPVIRSLTLEPDPPIVPGNVTLSVVGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCT 85
QY 101 DYIGSCTFHFCDVLDMLIPTGCPPEPLRTYGLPCHCPKSGTSLPKSEF 152
Db 86 DYIGSCTFHFCDVLDMLIPTGCPPEPLRTYGLPCHCPKSGTSLPKSEF 137

RESULT 2
US-09-183-841-1
; Sequence 1, Application US/09183841
; Patent No. 6423680
; GENERAL INFORMATION:
; APPLICANT: Hospital for Sick Children
; TITLE OF INVENTION: A No. 6423680el Inhibitor of Platelet Activating Factor
; FILE REFERENCE: vanz0010
; CURRENT APPLICATION NUMBER: US/09/183,841
; CURRENT FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 193

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (33)..(55)
; FEATURE:
; OTHER INFORMATION: residues 56-63 are included in a further precursor
; OTHER INFORMATION: form of the protein
US-09-183-841-1

Query Match      58.0%; Score 112; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 3.4e-102;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 EGKDPVIRSI...TLRPDPPIVPGNVTL...SVVGVSTSVPLSSPLKVDLVLEKEVAGWIKIPCT 100
Db 41 EGKDPVIRSI...TLRPDPPIVPGNVTL...SVVGVSTSVPLSSPLKVDLVLEKEVAGWIKIPCT 100

Qy 101 DYIGSCTFEHCVDVLDMLIPTGEPCEPLRTYGLPCHCPFKEGTYSLPKSEF 152
Db 101 DYIGSCTFEHCVDVLDMLIPTGEPCEPLRTYGLPCHCPFKEGTYSLPKSEF 152

RESULT 3
US-09-902-540-12082
; Sequence 12082, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12082
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12082

Query Match      5.2%; Score 10; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PLLIALGLLL 17
Db 231 PLLIALGLLL 240

RESULT 4
US-08-961-083-98
; Sequence 98, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2

Qy 8 PLLIALGLLL 17
Db 231 PLLIALGLLL 240
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; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 262 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-98

Query Match      4.7%; Score 9; DB 3; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 LSVVGSTSV 74
Db 155 LSVVGSTSV 163

RESULT 5
US-09-536-784-98
; Sequence 98, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 262 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-536-784-98

Query Match      4.7%; Score 9; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 LSVVGSTSV 74
Db 155 LSVVGSTSV 163

RESULT 6
US-09-961-083-206
; Sequence 206, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brooks, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-961-083-206

Query Match      4.7%; Score 9; DB 3; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 LSVVGSTSV 74
Db 163 LSVVGSTSV 171

RESULT 7
US-09-536-784-206
; Sequence 206, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-536-784-206

Query Match      4.7%; Score 9; DB 4; Length 270;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 LSVVGSTSV 74
Db 163 LSVVGSTSV 171

RESULT 8
US-09-583-110-4201
; Sequence 4201, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4201
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4201

Query Match      4.7%; Score 9; DB 4; Length 291;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      66 LSVVGSTSV 74
      |||||
Db      184 LSVVGSTSV 192

RESULT 9
US-09-107-433-3318
; Sequence 3318, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
;
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS: 5206
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3318:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...328
; SEQUENCE DESCRIPTION: SEQ ID NO: 3318:
US-09-107-433-3318

      Query Match      4.7%; Score 9; DB 4; Length 328;
      Best Local Similarity 100.0%; Pred. No. 1.1;
      Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 LSVVGSTSV 74
      |||||
Db      221 LSVVGSTSV 229

RESULT 10
US-09-949-016-6952
; Sequence 6952, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6952
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6952

      Query Match      4.1%; Score 8; DB 4; Length 390;
      Best Local Similarity 100.0%; Pred. No. 13;
      Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      86 LEKEVAGL 93
      |||||
Db      277 LEKEVAGL 284

RESULT 11
US-09-252-991A-20496
; Sequence 20496, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20496
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (31)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-20496

      Query Match      4.1%; Score 8; DB 4; Length 444;
      Best Local Similarity 100.0%; Pred. No. 15;
      Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 IALGLLLA 18
      |||||
Db      162 IALGLLLA 169

RESULT 12
US-09-252-991A-23790
; Sequence 23790, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
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; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23790
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23790

Query Match 4.1%; Score 8; DB 4; Length 563;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GLLLATPA 21
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Db 60 GLLLATPA 67

RESULT 13
US-09-320-878-12
; Sequence 12, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-320-878-12

Query Match 4.1%; Score 8; DB 3; Length 769;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GLLLATPA 21
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Db 285 GLLLATPA 292

RESULT 14
US-09-141-908-10
; Sequence 10, Application US/09141908
; Patent No. 6503741
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li

; TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a
; FILE REFERENCE: 300622002100
; CURRENT APPLICATION NUMBER: US/09/141,908
; CURRENT FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: PROV. 60/076,919
; EARLIER FILING DATE: 1998-03-05
; EARLIER APPLICATION NUMBER: PROV. 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-141-908-10

Query Match 4.1%; Score 8; DB 4; Length 769;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GLLLATPA 21
|||||||
Db 285 GLLLATPA 292

RESULT 15
US-09-657-440-12
; Sequence 12, Application US/09657440
; Patent No. 6509455
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/657,440
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/320,878
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: CIP OF 09/141,908
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 769
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-657-440-12

Query Match 4.1%; Score 8; DB 4; Length 769;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GLLLATPA 21
|||||||
Db 285 GLLLATPA 292

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OM protein - protein search, using sw model

Run on: July 27, 2005, 19:08:40 ; Search time 107.222 Seconds
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	112	58.0	193	15	US-10-170-385-389 Sequence 389, App
2	112	58.0	193	16	US-10-723-860-529 Sequence 529, App
3	61	31.6	61	9	US-09-864-761-34809 Sequence 34809, A
4	11	5.7	11	9	US-09-791-378-579 Sequence 579, App
5	11	5.7	11	11	US-09-791-377-579 Sequence 579, App
6	9	4.7	262	9	US-09-765-272-98 Sequence 98, Appl
7	9	4.7	291	9	US-09-765-272-206 Sequence 206, App
8	9	4.7	291	17	US-10-472-928-4348 Sequence 4348, Ap
9	9	4.7	328	18	US-10-617-320-3318 Sequence 3318, Ap
10	8	4.1	8	9	US-09-791-378-578 Sequence 578, App
11	8	4.1	8	11	US-09-791-377-578 Sequence 578, App

12	8	4.1	100	15	US-10-424-599-228216 Sequence 228216,
13	8	4.1	110	16	US-10-425-115-305533 Sequence 305333,
14	8	4.1	170	10	US-09-804-014A-37 Sequence 37, Appl
15	8	4.1	323	16	US-10-739-930-5722 Sequence 5722, Ap
16	8	4.1	466	16	US-10-437-963-119990 Sequence 119990,
17	8	4.1	574	16	US-10-324-967-36 Sequence 36, Appl
18	8	4.1	589	15	US-10-424-599-245422 Sequence 245422,
19	8	4.1	769	10	US-09-793-708-12 Sequence 12, Appl
20	8	4.1	769	14	US-10-201-365-10 Sequence 10, Appl
21	8	4.1	769	14	US-10-160-539-12 Sequence 12, Appl
22	8	4.1	769	17	US-10-468-828-12 Sequence 12, Appl
23	8	4.1	809	9	US-09-861-289-24 Sequence 24, Appl
24	8	4.1	809	9	US-09-860-846-24 Sequence 24, Appl
25	8	4.1	809	10	US-09-988-384B-24 Sequence 24, Appl
26	8	4.1	809	10	US-09-836-821-24 Sequence 24, Appl
27	8	4.1	809	14	US-10-271-889-24 Sequence 24, Appl
28	8	4.1	809	16	US-10-398-605-24 Sequence 24, Appl
29	8	4.1	1308	16	US-10-437-963-186215 Sequence 186215,
30	8	4.1	3782	9	US-09-861-289-4 Sequence 4, Appl
31	8	4.1	3782	9	US-09-860-846-4 Sequence 4, Appl
32	8	4.1	3782	10	US-09-988-384B-4 Sequence 4, Appl
33	8	4.1	3782	10	US-09-836-821-4 Sequence 4, Appl
34	8	4.1	3782	14	US-10-271-889-47 Sequence 47, Appl
35	8	4.1	3782	16	US-10-398-605-4 Sequence 4, Appl
36	7	3.6	23	17	US-10-828-559-3 Sequence 3, Appl
37	7	3.6	39	11	US-09-833-245-1222 Sequence 1222, Ap
38	7	3.6	39	11	US-09-833-245-1224 Sequence 1224, Ap
39	7	3.6	53	15	US-10-424-599-268608 Sequence 268608,
40	7	3.6	54	16	US-10-425-115-220040 Sequence 220040,
41	7	3.6	60	15	US-10-424-599-208921 Sequence 208921,
42	7	3.6	60	15	US-10-424-599-241819 Sequence 241819,
43	7	3.6	73	14	US-10-106-698-6961 Sequence 6961, Ap
44	7	3.6	83	15	US-10-425-114-61932 Sequence 61932, A
45	7	3.6	84	16	US-10-425-115-202828 Sequence 202828,

ALIGNMENTS

RESULT 1

US-10-170-385-389
; Sequence 389, Application US/10170385
; Publication No. US2003020372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-389

Query Match 58.0%; Score 112; DB 15; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.9e-99;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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; SEQ ID NO 579
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-579

Query Match      5.7%; Score 11; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      131 TYGLPCHCPEK 141
Db      1 TYGLPCHCPEK 11
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RESULT 5
US-09-791-377-579
; Sequence 579, Application US/09791377
; Publication No. US20040110939A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 579
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-377-579

Query Match      5.7%; Score 11; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      131 TYGLPCHCPEK 141
Db      1 TYGLPCHCPEK 11
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RESULT 6
US-09-765-272-98
; Sequence 98, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-765-272-206

Query Match      4.7%; Score 9; DB 9; Length 270;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 LSVGVSTSV 74
Db      155 LSVGVSTSV 163
|||||

RESULT 7
US-09-765-272-206
; Sequence 206, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-09-765-272-206

Query Match      4.7%; Score 9; DB 9; Length 270;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 LSVGVSTSV 74
Db      155 LSVGVSTSV 163
|||||

NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-765-272-98

Query Match      4.7%; Score 9; DB 9; Length 262;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      66 LSVGVSTSV 74
Db      155 LSVGVSTSV 163
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Qy 66 LSVVGSTSV 74
    |||||
Db 163 LSVVGSTSV 171

RESULT 8
US-10-472-928-4348
; Sequence 4348, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SA
; TITLE OF INVENTION: THE INSTITUTE FOR GENOMIC RESEARCH
; FILE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926W0
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4348
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; OTHER INFORMATION: phosphate ABC transporter, phosphate-binding protein (psts)
; OTHER INFORMATION: Cellular location: lipoprotein
; OTHER INFORMATION: Similar to strain R6 sequence 15903936 (e-160)
US-10-472-928-4348

Query Match 4.7%; Score 9; DB 17; Length 291;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 LSVVGSTSV 74
    |||||
Db 184 LSVVGSTSV 192

RESULT 9
US-10-617-320-3318
; Sequence 3318, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/617,320
; FILING DATE: 10-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
```

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;
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3318:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...328
; SEQUENCE DESCRIPTION: SEQ ID NO: 3318:
US-10-617-320-3318

Query Match 4.7%; Score 9; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 LSVVGSTSV 74
    |||||
Db 221 LSVVGSTSV 229

RESULT 10
US-09-791-378-578
; Sequence 578, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 578
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-578

Query Match 4.1%; Score 8; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 89 EVAGLWIK 96
    |||||
Db 1 EVAGLWIK 8

RESULT 11
US-09-791-377-578
; Sequence 578, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
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; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 578

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-377-578

Query Match 4.1%; Score 8; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 89 EVAGLWIK 96

Db 1 EVAGLWIK 8

RESULT 12

US-10-424-599-228216

; Sequence 228216, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 228216

; LENGTH: 100

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_48107C.1.pap

US-10-424-599-228216

Query Match 4.1%; Score 8; DB 15; Length 100;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 STSVPLSS 78

Db 10 STSVPLSS 17

RESULT 13

US-10-425-115-305353

; Sequence 305353, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 305353

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_41551C.1.pap

US-10-425-115-305353

Query Match 4.1%; Score 8; DB 16; Length 110;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 IRSLTLEP 55

Db 19 IRSLTLEP 26

RESULT 14

US-09-804-014A-37

; Sequence 37, Application US/09804014A

; Publication No. US20030064489A1

; GENERAL INFORMATION:

; APPLICANT: Li, Li

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Vernet, Corine

; APPLICANT: Fernandes, Elma

; APPLICANT: Shimkets, Richard

; APPLICANT: Spaderna, Steven

; APPLICANT: Majumder, Kumud

; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same

; FILE REFERENCE: 15966-721 US

; CURRENT APPLICATION NUMBER: US/09/804,014A

; CURRENT FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/188,316

; PRIOR FILING DATE: 2000-03-10

; PRIOR APPLICATION NUMBER: 60/188,277

; PRIOR FILING DATE: 2000-03-10

; PRIOR APPLICATION NUMBER: 60/189,139

; PRIOR FILING DATE: 2000-03-14

; PRIOR APPLICATION NUMBER: 60/189,140

; PRIOR FILING DATE: 2000-03-14

; PRIOR APPLICATION NUMBER: 60/190,401

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/190,231

; PRIOR FILING DATE: 2000-03-17

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 37

; LENGTH: 170

; TYPE: PRT

; ORGANISM: Bos taurus

US-09-804-014A-37

Query Match 4.1%; Score 8; DB 10; Length 170;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 LEKEVAGL 93

Db 107 LEKEVAGL 114

RESULT 15

US-10-739-930-5722

; Sequence 5722, Application US/10739930

; Publication No. US20040216190A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

; FILE REFERENCE: 38-21(53377)B

; CURRENT APPLICATION NUMBER: US/10/739,930

; CURRENT FILING DATE: 2003-12-18

; NUMBER OF SEQ ID NOS: 11088

; SEQ ID NO 5722

; LENGTH: 323

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

; FEATURE:

; OTHER INFORMATION: Clone ID: ARATH-23APR03-C126388_1.p

US-10-739-930-5722

Query Match

4.1%; Score 8; DB 16; Length 323;

Best Local Similarity 100.0%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 LEKEVAGL 93
Db 149 LEKEVAGL 156

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OM protein - nucleic search, using frame_plus_p2n model

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Perfect score: 94
Sequence: 1 FSWNCFEGKPAVIR 16

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	90.4	546	13	US-10-027-632-207798 Sequence 207798,
2	85	90.4	546	13	US-10-027-632-207799 Sequence 207799,
3	85	90.4	546	13	US-10-027-632-207800 Sequence 207800,
4	85	90.4	546	13	US-10-027-632-207801 Sequence 207801,
5	85	90.4	546	17	US-10-027-632-207798 Sequence 207798,
6	85	90.4	546	17	US-10-027-632-207799 Sequence 207799,
7	85	90.4	546	17	US-10-027-632-207800 Sequence 207800,
8	85	90.4	546	17	US-10-027-632-207801 Sequence 207801,
9	85	90.4	528	20	US-10-723-860-528 Sequence 528, App
10	85	90.4	1935	10	US-09-971-392-102 Sequence 102, App
11	85	90.4	2384	9	US-09-822-849A-53 Sequence 53, Appl
12	85	90.4	2436	9	US-09-954-531-380 Sequence 380, Appl
13	85	90.4	2436	10	US-09-525-978B-81 Sequence 81, Appl
14	85	90.4	2436	21	US-10-843-641A-1447 Sequence 1447, Ap
15	85	90.4	2478	17	US-10-170-385-390 Sequence 390, App
16	85	90.4	3988	20	US-10-723-860-5187 Sequence 5187, Ap
17	82	87.2	1983	17	US-10-388-934-167 Sequence 167, App
C 18	58	61.7	857	13	US-10-027-632-164063 Sequence 164063,
C 19	58	61.7	857	13	US-10-027-632-164064 Sequence 164064,
C 20	58	61.7	857	13	US-10-027-632-164065 Sequence 164065,
C 21	58	61.7	857	17	US-10-027-632-164063 Sequence 164063,
C 22	58	61.7	857	17	US-10-027-632-164064 Sequence 164064,
C 23	58	61.7	857	17	US-10-027-632-164065 Sequence 164065,
C 24	57	60.6	380	10	US-09-764-891-2290 Sequence 2290, Ap
25	57	60.6	577	17	US-10-264-049-436 Sequence 436, App
26	55	58.5	580	13	US-10-027-632-91348 Sequence 91348, A
27	55	58.5	580	13	US-10-027-632-317712 Sequence 317712,
28	55	58.5	580	17	US-10-027-632-91348 Sequence 91348, A
29	55	58.5	580	17	US-10-027-632-317712 Sequence 317712,
30	50.5	53.7	400660	19	US-10-388-838-68 Sequence 68, Appl
31	50	53.2	2243	17	US-10-108-260A-301 Sequence 301, App
C 32	50	53.2	2367	18	US-10-267-502-81 Sequence 81, Appl
C 33	50	53.2	2452	17	US-10-094-749-87 Sequence 87, Appl
C 34	50	53.2	383432	22	US-10-737-082-34 Sequence 34, Appl
C 35	50	53.2	383432	22	US-10-765-790-34 Sequence 34, Appl
C 36	49.5	52.7	600	22	US-10-972-079-45839 Sequence 45839, A
37	49	52.1	653	13	US-10-027-632-121823 Sequence 121823,
38	49	52.1	653	17	US-10-027-632-121823 Sequence 121823,
C 39	49	52.1	1197	18	US-10-424-599-20544 Sequence 20544, A
C 40	49	52.1	1493	18	US-10-424-599-78156 Sequence 78156, A
C 41	49	52.1	1701	18	US-10-335-977-3769 Sequence 3769, Ap
C 42	49	52.1	1704	18	US-10-335-977-3768 Sequence 3768, Ap
C 43	49	52.1	6306	18	US-10-433-794-38 Sequence 38, Appl
C 44	49	52.1	6629	17	US-10-353-690-35 Sequence 35, Appl
C 45	49	52.1	6629	17	US-10-172-118-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-027-632-207798
; Sequence 207798, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIORITY FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIORITY FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIORITY FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483

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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207798
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207798

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 13 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207798 (1-546)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
Db 276 TTTTCTGGGATACTGTGATGAAGGAGGACCTCGCGGTGATCAGA 323

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RESULT 2
US-10-027-632-207798
; Sequence 207799, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207799
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207799

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 13 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207799 (1-546)

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Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
Db 276 TTTTCTGGGATACTGTGATGAAGGAGGACCTCGCGGTGATCAGA 323

RESULT 3
US-10-027-632-207800
; Sequence 207800, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207800
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207800

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 13 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207800 (1-546)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
Db 276 TTTTCTGGGATACTGTGATGAAGGAGGACCTCGCGGTGATCAGA 323

RESULT 4
US-10-027-632-207801
; Sequence 207801, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23

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; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207801
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207801

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 13 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207801 (1-546)

Qy 1 PheSerTrpAspAenCysPheGluGlyLysAspProAlaValIleArg 16
|||||
Db 276 TTTTCTGGGATAACTGTGATGAGGAGGACCTCGCGTGATCAGA 323

RESULT 5

US-10-027-632-207798
; Sequence 207798, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207798

; LENGTH: 546

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-207798

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207798 (1-546)

Qy 1 PheSerTrpAspAenCysPheGluGlyLysAspProAlaValIleArg 16
|||||
Db 276 TTTTCTGGGATAACTGTGATGAGGAGGACCTCGCGTGATCAGA 323

RESULT 6

US-10-027-632-207799
; Sequence 207799, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207799

; LENGTH: 546

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-207799

Alignment Scores:

Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207799 (1-546)

Qy 1 PheSerTrpAspAenCysPheGluGlyLysAspProAlaValIleArg 16
|||||
Db 276 TTTTCTGGGATAACTGTGATGAGGAGGACCTCGCGTGATCAGA 323

RESULT 7

US-10-027-632-207800
; Sequence 207800, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720

; LENGTH: 546

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-207798

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207798 (1-546)

Qy 1 PheSerTrpAspAenCysPheGluGlyLysAspProAlaValIleArg 16
|||||
Db 276 TTTTCTGGGATAACTGTGATGAGGAGGACCTCGCGTGATCAGA 323

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207800
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207800

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207800 (1-546)

Qy 1 PheSerTrpAspAsnCysPheGluGlyAspProAlaValIleArg 16
Db 276 TTTTCCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 323

RESULT 8
US-10-027-632-207801
; Sequence 207801, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207801
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207801

Alignment Scores:
Pred. No.: 1.82e-05 Length: 546
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-68 (1-16) x US-10-027-632-207801 (1-546)

Qy 1 PheSerTrpAspAsnCysPheGluGlyAspProAlaValIleArg 16
Db 276 TTTTCCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 323

RESULT 9
US-10-723-860-528
; Sequence 528, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
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; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 528
; LENGTH: 953
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-528

Alignment Scores:
Pred. No.: 3.39e-05 Length: 953
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 20 Gaps: 0

US-10-030-937-68 (1-16) x US-10-723-860-528 (1-953)

Qy 1 PheSerTrpAspAsnCysPheGluGlyAspProAlaValIleArg 16
Db 190 TTTTCCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 237

RESULT 10
US-09-971-392-102
; Sequence 102, Application US/09971392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, David P.
; APPLICANT: Pearson, Cecelia I.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 102
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Template ID: 977615.8
US-09-971-392-102

Alignment Scores:
Pred. No.: 7.46e-05 Length: 1935
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 10 Gaps: 0

US-10-030-937-68 (1-16) x US-09-971-392-102 (1-1935)

Qy 1 PheSerTrpAspAsnCysPheGluGlyAspProAlaValIleArg 16
Db 201 TTTTCCTGGGATAACTGTGATGAAGGAAGGACCCCTGCGGTGATCAGA 248

RESULT 11
US-09-822-849A-53
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; Sequence 53, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fecthel, Kim
; APPLICANT: Acostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-53

Alignment Scores:
Pred. No.: 9.41e-05 Length: 2384
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: Gaps: 0

US-10-030-937-68 (1-16) x US-09-822-849A-53 (1-2384)

QY 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
Db 112 TTTTCTGGGATACTGTGATGAAGGAAGGACCTCGCGTGATCAGA 159

RESULT 12

US-09-954-531-380
; Sequence 380, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 380
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-380

Alignment Scores:
Pred. No.: 9.64e-05 Length: 2436
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0

Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: Gaps: 0
US-10-030-937-68 (1-16) x US-09-954-531-380 (1-2436)

QY 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
Db 158 TTTTCTGGGATACTGTGATGAAGGAAGGACCTCGCGTGATCAGA 205

RESULT 13

US-09-525-978B-81
; Sequence 81, Application US/09525978B
; Publication No. US20030049722A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Caras, Ingrid W.
; APPLICANT: Hevezi, Peter
; APPLICANT: Wilson, Keith
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING MACROPHAGE DEVELOPMENT
; TITLE OF INVENTION: RELATED DISORDERS, COMPOSITIONS, AND METHODS OF
; TITLE OF INVENTION: SCREENING FOR MACROPHAGE DEVELOPMENT MODULATORS
; FILE REFERENCE: A-67413-1/DJB/JJD
; CURRENT APPLICATION NUMBER: US/09/525,978B
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: USSN 60/124,530
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-978B-81

Alignment Scores:
Pred. No.: 9.64e-05 Length: 2436
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: Gaps: 0
US-10-030-937-68 (1-16) x US-09-525-978B-81 (1-2436)

QY 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
Db 158 TTTTCTGGGATACTGTGATGAAGGAAGGACCTCGCGTGATCAGA 205

RESULT 14

US-10-843-641A-1447
; Sequence 1447, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768

;
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1447
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-1447

Alignment Scores:
Pred. No.: 9.64e-05 Length: 2436
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 21 Gaps: 0

US-10-030-937-68 (1-16) x US-10-843-641A-1447 (1-2436)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
Db 158 TTTTCTGGGATACTGTGATGAAGGAAGACCCCTGGGTGATCAGA 205

RESULT 15

US-10-170-385-390
; Sequence 390, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-390

Alignment Scores:
Pred. No.: 9.82e-05 Length: 2478
Score: 85.00 Matches: 15
Percent Similarity: 93.75% Conservative: 0
Best Local Similarity: 93.75% Mismatches: 1
Query Match: 90.43% Indels: 0
DB: 17 Gaps: 0

US-10-030-937-68 (1-16) x US-10-170-385-390 (1-2478)

Qy 1 PheSerTrpAspAsnCysPheGluGlyLysAspProAlaValIleArg 16
|||||

Db 195 TTTTCTGGGATACTGTGATGAAGGAAGACCCCTGGGTGATCAGA 242

Search completed: July 27, 2005, 22:48:02
Job time : 100.631 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 19:27:35 ; Search time 312.231 Seconds
(without alignments)
1011.435 Million cell updates/sec

Title: US-10-030-937-9
Perfect score: 193
Sequence: 1 MSLMQAPLLIALLLLATP.....LSSSGKRLGCIKIAASLKGI 193

Scoring table:

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2400006

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO.spool/US1003937/runat 26072005 132301 10709/app query.fasta 1.789
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2noli.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US1003937 @CGN 1 1 116 @runat 26072005 132301 10709 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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2:	/cgn2_6/ptodata/1/ina/5B COMB.seq:*
3:	/cgn2_6/ptodata/1/ina/6A COMB.seq:*
4:	/cgn2_6/ptodata/1/ina/6B COMB.seq:*
5:	/cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
6:	/cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	5.2	1089	4	US-09-902-540-4802
2	10	5.2	29103	4	US-09-902-540-1236
3	9	4.7	787	3	US-08-961-083-97
4	9	4.7	787	4	US-09-536-784-97
5	9	4.7	811	3	US-08-961-083-205
6	9	4.7	811	4	US-09-536-784-205
7	9	4.7	876	4	US-09-583-110-1540
8	9	4.7	987	4	US-09-107-433-715
9	9	4.7	12127	3	US-08-961-527-148
10	9	4.7	48794	4	US-09-949-016-15637
11	8	4.1	462	4	US-09-252-991A-546
12	8	4.1	601	4	US-09-949-016-39132

13	8	4.1	601	4	US-09-949-016-53584	Sequence 53584, A
14	8	4.1	601	4	US-09-949-016-61592	Sequence 61592, A
15	8	4.1	601	4	US-09-949-016-61593	Sequence 61593, A
16	8	4.1	601	4	US-09-949-016-61714	Sequence 61714, A
17	8	4.1	601	4	US-09-949-016-61715	Sequence 61715, A
18	8	4.1	601	4	US-09-949-016-84688	Sequence 84688, A
19	8	4.1	601	4	US-09-949-016-91993	Sequence 91993, A
20	8	4.1	601	4	US-09-949-016-91994	Sequence 91994, A
21	8	4.1	601	4	US-09-949-016-158399	Sequence 158399, A
22	8	4.1	601	4	US-09-949-016-158400	Sequence 158400, A
23	8	4.1	711	4	US-09-774-639-24	Sequence 24, Appl
24	8	4.1	858	4	US-09-252-991A-3981	Sequence 3981, Ap
25	8	4.1	1314	4	US-09-252-991A-7168	Sequence 7168, Ap
26	8	4.1	1335	4	US-09-252-991A-3925	Sequence 3925, Ap
27	8	4.1	1395	4	US-09-711-161-270	Sequence 270, App
28	8	4.1	1395	4	US-09-492-709A-121	Sequence 121, App
29	8	4.1	1456	3	US-09-308-406-1	Sequence 1, Appl
30	8	4.1	1458	4	US-09-252-991A-570	Sequence 570, App
31	8	4.1	1482	4	US-09-252-991A-4050	Sequence 4050, App
32	8	4.1	1605	4	US-09-252-991A-3897	Sequence 3897, Ap
33	8	4.1	1677	4	US-09-252-991A-7476	Sequence 7476, Ap
34	8	4.1	1692	4	US-09-252-991A-7219	Sequence 7219, Ap
35	8	4.1	2223	4	US-09-252-991A-4015	Sequence 4015, Ap
36	8	4.1	2401	3	US-09-320-878-20	Sequence 20, Appl
37	8	4.1	2401	4	US-09-141-908-9	Sequence 9, Appl
38	8	4.1	2401	4	US-09-657-440-20	Sequence 20, Appl
39	8	4.1	2430	3	US-09-105-537-23	Sequence 23, Appl
40	8	4.1	2772	3	US-08-936-135-1	Sequence 1, Appl
41	8	4.1	2772	4	US-09-439-711C-1	Sequence 1, Appl
42	8	4.1	2881	2	US-08-570-227A-1	Sequence 1, Appl
43	8	4.1	2881	3	US-09-077-991-1	Sequence 1, Appl
44	8	4.1	3125	4	US-09-949-016-1081	Sequence 1081, Ap
45	8	4.1	3241	3	US-09-434-288-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-902-540-4802
; Sequence 4802, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4802
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4802

Alignment Scores:
Pred. No.: 0.86 Length: 1089
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-902-540-4802 (1-1089)

Qy 8 ProLeuLeuLeuAlaLeuGlyLeuLeuLeu 17

Db 691 CCGCTGCTCATCGCCCTGGGCTGCTGCTG 720

RESULT 2
US-09-902-540-1236
; Sequence 1236, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1236
; LENGTH: 29103
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(29103)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1236

Alignment Scores:
Pred. No.: 21, 2 Length: 29103
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-902-540-1236 (1-29103)

Qy 8 ProLeuLeuAlaLeuGlyLeuLeu 17
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Db 18065 CCGCTGCTCATCGCCCTGGCGCTGCTGCTG 18094

RESULT 3
US-08-961-083-97
; Sequence 97, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504

1.33

Alignment Scores:	
Pred. NO.:	7.53
Length:	876

Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-583-110-1540 (1-876)

Qy 66 LeuSerValValGlySerThrSerVal 74
Db 550 TTGTCGTGTAGTCCACTTCAGTA 576

RESULT 8
US-09-107-433-715
; Sequence 715, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIORITY INFORMATION:
; PRIOR APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 715:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...987
; SEQUENCE DESCRIPTION: SEQ ID NO: 715:
US-09-107-433-715
Alignment Scores:
Pred. No.: 8.46 Length: 987
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-107-433-715 (1-987)

Qy 66 LeuSerValValGlySerThrSerVal 74
Db 661 TTGTCGTGTAGTCCACTTCAGTA 687

RESULT 9
US-08-961-527-148
; Sequence 148, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12127 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-148
Alignment Scores:
Pred. No.: 97.8 Length: 12127
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 3 Gaps: 0

US-10-030-937-9 (1-193) x US-08-961-527-148 (1-12127)

Qy 66 LeuSerValValGlySerThrSerVal 74
Db 624 TTGTCGTGTAGTCCACTTCAGTA 650

RESULT 10
US-09-949-016-15637
; Sequence 15637, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15637
; LENGTH: 48794
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(48794)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15637

Alignment Scores:
Pred. No.: 380 Length: 48794
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.66% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-949-016-15637 (1-48794)

QY 71 SerThrSerValProLeuSerPro 79
Db 37782 TCACCTCAGTTCCTTTATCTTCTCT 37808

RESULT 11
US-09-252-991A-546/c
; Sequence 546, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 546
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-546

Alignment Scores:
Pred. No.: 43.7 Length: 462
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.15% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-252-991A-546 (1-462)

QY 71 SerThrSerValProLeuSerPro 78
Db 395 TCTACGTCAGTTCCTTTTCGTCA 372

RESULT 12
US-09-949-016-39132
; Sequence 39132, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39132
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-39132

Alignment Scores:
Pred. No.: 56.5 Length: 601
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.15% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-949-016-39132 (1-601)

QY 86 LeuGluLysGluValAlaGlyLeu 93
Db 188 CTGGAAGAGGAGTCCCGGGTTG 211

RESULT 13
US-09-949-016-53584
; Sequence 53584, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53584
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-53584

Alignment Scores:
Pred. No.: 56.5 Length: 601
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.15% Indels: 0
DB: 4 Gaps: 0

US-10-030-937-9 (1-193) x US-09-949-016-53584 (1-601)

QY 175 SerSerSerGlyLeuArgLeuGly 182
Db 173 TCAACGTCAGTGAAGAGGCTGGC 196
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RESULT 14
US-09-949-016-61592
; Sequence 61592, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61592
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-61592

Alignment Scores:
Pred. No.:      56.5      Length:      601
Score:          8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      4.15%      Indels:      0
DB:               4      Gaps:      0

US-10-030-937-9 (1-193) x US-09-949-016-61592 (1-601)
Qy      67 SerValValGlySerThrSerVal 74
Db      475 TCCGTCGTTGGGTCACCAGTG 498

RESULT 15
US-09-949-016-61593
; Sequence 61593, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61593
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-61593

Alignment Scores:
Pred. No.:      56.5      Length:      601
Score:          8.00      Matches:      8
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      4.15%      Indels:      0
DB:               4      Gaps:      0
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US-10-030-937-9 (1-193) x US-09-949-016-61593 (1-601)
Qy      67 SerValValGlySerThrSerVal 74
Db      227 TCCGTCGTTGGGTCACCAGTG 250

Search completed: July 27, 2005, 22:54:19
Job time : 323.231 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 27, 2005, 22:24:57 ; Search time 1189.74 Seconds
(without alignments)
1048.964 Million cell updates/sec

Title: US-10-030-937-9

Perfect score: 193

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7277826 seqs, 3233139505 residues

Word size: 1

Total number of hits satisfying chosen parameters: 14544430

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=Published Applications NA -QWMT=fastap -SUPPFX=p2noli.rnpb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HSP SIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USRR=US10030937 @CGN 1.1.684 @runat_26072005_132302_10742
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-XGAPOP=6 -XGAPEXT=7 -XGAPOP=60 -XGAPEXT=60 -DELOP=6 -DELEXT=7

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- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
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- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	112	58.0	953	20	US-10-723-860-528	Sequence 528, App
2	112	58.0	1935	10	US-09-971-392-102	Sequence 102, App
3	112	58.0	2384	9	US-09-823-849A-53	Sequence 53, Appl
4	112	58.0	2436	9	US-09-954-531-380	Sequence 380, App
5	112	58.0	2436	10	US-09-525-978B-81	Sequence 81, Appl
6	112	58.0	2436	21	US-10-843-641A-1447	Sequence 1447, Ap
7	112	58.0	2478	17	US-10-170-385-390	Sequence 390, App
8	112	58.0	3988	20	US-10-723-860-5187	Sequence 5187, Ap
9	61	31.6	475	9	US-09-864-761-1518	Sequence 1518, Ap
10	48	24.9	145	9	US-09-864-761-18277	Sequence 18277, A
11	40	20.7	448	11	US-09-959-034-4215	Sequence 4215, Ap
12	40	20.7	25000	16	US-10-225-810-26	Sequence 26, Appl
13	18	9.3	546	13	US-10-027-632-207798	Sequence 207798,
14	18	9.3	546	13	US-10-027-632-207799	Sequence 207799,
15	18	9.3	546	13	US-10-027-632-207800	Sequence 207800,
16	18	9.3	546	13	US-10-027-632-207801	Sequence 207801,
17	18	9.3	546	17	US-10-027-632-207798	Sequence 207798,
18	18	9.3	546	17	US-10-027-632-207799	Sequence 207799,
19	18	9.3	546	17	US-10-027-632-207800	Sequence 207800,
20	18	9.3	546	17	US-10-027-632-207801	Sequence 207801,
21	18	9.3	1983	17	US-10-388-934-167	Sequence 167, App
22	9	4.7	218	11	US-09-922-293-2287	Sequence 2287, Ap
23	9	4.7	455	13	US-10-027-632-202246	Sequence 202246,
24	9	4.7	455	17	US-10-027-632-202246	Sequence 202246,
25	9	4.7	649	18	US-10-425-114-7785	Sequence 7785, Ap
26	9	4.7	787	9	US-09-765-272-97	Sequence 97, Appl
27	9	4.7	811	9	US-09-765-272-205	Sequence 205, App
28	9	4.7	873	21	US-10-472-928-4347	Sequence 4347, Ap
29	9	4.7	987	22	US-10-617-320-715	Sequence 715, App
30	9	4.7	1051	18	US-10-424-599-38496	Sequence 38496, A
31	9	4.7	12127	8	US-08-961-527-148	Sequence 148, App
32	9	4.7	12127	17	US-10-158-844-148	Sequence 148, App
33	9	4.7	2162598	21	US-10-472-928-4979	Sequence 4979, Ap
34	8	4.1	25	21	US-10-719-900-237828	Sequence 237828, Ap
35	8	4.1	60	10	US-09-908-975-22643	Sequence 22643, A
36	8	4.1	195	9	US-09-864-761-18267	Sequence 18267, A
37	8	4.1	223	18	US-10-424-599-102858	Sequence 102858,
38	8	4.1	274	20	US-10-425-115-5227	Sequence 5227, Ap
39	8	4.1	301	21	US-10-696-639-2552	Sequence 2552, Ap
40	8	4.1	319	9	US-09-864-761-20513	Sequence 20513, A
41	8	4.1	331	20	US-10-425-115-120690	Sequence 120690,
42	8	4.1	391	11	US-09-864-408A-4241	Sequence 4241, Ap
43	8	4.1	406	9	US-09-960-352-14056	Sequence 14056, A
44	8	4.1	420	18	US-10-424-599-85374	Sequence 85374, A
45	8	4.1	430	9	US-09-864-761-1508	Sequence 1508, Ap

ALIGNMENTS

RESULT 1

US-10-723-860-528
; Sequence 528, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NFUS01
; CURRENT APPLICATION NUMBER: US/10723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 528

; LENGTH: 953

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-860-528

Alignment Scores:

Pred. No.: 1.63e-102 Length: 953
Score: 112.00 Matches: 152
Percent Similarity: 98.70% Conservative: 0
Best Local Similarity: 98.70% Mismatches: 1
Query Match: 58.03% Indels: 2
DB: 20 Gaps: 0

US-10-030-937-9 (1-193) x US-10-723-860-528 (1-953)

QY 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
DB 211 GAAGGGAAGGACCTCGCGTGATCAGAAAGCTGACTGTGGAGCTGACCCCATCGTCGTT 270
QY 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
DB 271 CCTGGAATGTGACCTTCAGTGTGCGGAGCAGCAGTGTCCCTGAGTTCTCTCTG 330
QY 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
DB 331 AAGTGGATTAGTTTGGAGAGGAGGTGGCTCTGGATCAAGATCCCATGCACA 390
QY 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
DB 391 GACTACATTGGCAGCTGACTTGAACACTTCTGTGATGTGCTTGAATTCCT 450
QY 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
DB 451 ACTGGGAGCCCTGCCAGAGCCCTGCGTACCTATGGGCTTCTTGCACATGTCCTTC 510
QY 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuPr 160
DB 511 AAAGAGGAACCTACTACTGCCCAAGAGGAAATCGT-TGTGCTTGACCTGGAGCTGCC 569
QY 160 oSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysAr 180
DB 570 CAGTTGGCTCACCACCGGAACTACCGCATAGAGAGCGTCTCGAGCAGCAGTGGGAAGCG 629
QY 180 gLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
DB 630 TCTGGGCTGCATCAAGATCGCTGCTCTCTAAAGGGGCATA 669

RESULT 2

US-09-971-392-102

; Sequence 102, Application US/09971392

; Publication No. US20030134283A1

; GENERAL INFORMATION:

; APPLICANT: Peterson, David P.

; APPLICANT: Pearson, Cecelia I.

; APPLICANT: Cocks, Benjamin G.

; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION

; FILE REFERENCE: PA-0029 US

; CURRENT APPLICATION NUMBER: US/09/971,392

; CURRENT FILING DATE: 2001-10-03

; PRIOR APPLICATION NUMBER: 60/237,652

; PRIOR FILING DATE: 2000-10-03

; NUMBER OF SEQ ID NOS: 260

; SOFTWARE: PERL Program

; SEQ ID NO 102

; LENGTH: 1935

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Template ID: 977615.8

US-09-971-392-102

Alignment Scores:

Pred. No.: 3.08e-102 Length: 1935
Score: 112.00 Matches: 152
Percent Similarity: 98.70% Conservative: 0
Best Local Similarity: 98.70% Mismatches: 1
Query Match: 58.03% Indels: 2
DB: 10 Gaps: 0

US-10-030-937-9 (1-193) x US-09-971-392-102 (1-1935)

QY 41 GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal 60
DB 222 GAAGGGAAGGACCTCGCGTGATCAGAAAGCTGACTGTGGAGCCTGACCCCATCGTCGTT 281
QY 61 ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu 80
DB 282 CTGGAATGTGACCTTCAGTGTGCGGAGCAGCAGTGTCCCTGAGTTCTCTCTG 341
QY 81 LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr 100
DB 342 AAGTGGATTAGTTTGGAGAGGAGGTGGCTCTGGATCAAGATCCCATGCACA 401
QY 101 AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro 120
DB 402 GACTACATTGGCAGCTGACTTGAACACTTCTGTGATGTGCTTGAATTCCT 461
QY 121 ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe 140
DB 462 ACTGGGAGCCCTGCCAGAGCCCTGCGTACCTATGGGCTTCTTGCACATGTCCTTC 521
QY 141 LysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuPr 160
DB 522 AAAGAGGAACCTACTACTGCCCAAGAGGAAATCGT-TGTGCTTGACCTGGAGCTGCC 580
QY 160 oSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysAr 180
DB 581 CAGTTGGCTCACCACCGGAACTACCGCATAGAGAGCGTCTCGAGCAGCAGTGGGAAGCG 640
QY 180 gLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
DB 641 TCTGGGCTGCATCAAGATCGCTGCTCTCTAAAGGGGCATA 680

RESULT 3

US-09-822-849A-53

; Sequence 53, Application US/09822849A

; Patent No. US20020045170A1

; GENERAL INFORMATION:

; APPLICANT: Wong, Gordon G.

; APPLICANT: Clark, Hilary

; APPLICANT: Fechtel, Kim

; APPLICANT: Agostino, Michael J.

; APPLICANT: Howes, Steven H.

; APPLICANT: Resnick, Richard J.

; APPLICANT: Gulukota, Kamalakar

; APPLICANT: Graham, James R.

; APPLICANT: Genetics Institute, Inc.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

; FILE REFERENCE: GIN 6403

; CURRENT APPLICATION NUMBER: US/09/822,849A

; CURRENT FILING DATE: 2001-09-04

; PRIOR APPLICATION NUMBER: 60/195,582

; PRIOR FILING DATE: 2000-04-06

; NUMBER OF SEQ ID NOS: 598

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 53

; LENGTH: 2384

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-822-849A-53

Alignment Scores:

Pred. No.: 3.72e-102 Length: 2384

Score:	112.00	Matches:	191
Percent Similarity:	97.95%	Conservative:	0
Best Local Similarity:	97.95%	Mismatches:	2
Query Match:	58.03%	Indels:	4
DB:	10	Gaps:	0

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Qy	1	MetGlnSerLeuMetGlnAlaProLeuLeuLeuAlaLeuLeuLeuLeuAlaThrPro	20
Db	59	ATGCAGTCCCTGATGCAGGCTCCCTCTGATCGCCCTGGCTTGTCTTCGGGACCCCT	118
Qy	21	AlaGlnAlaHisLeuLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe	40
Db	119	GCGCAAGCCACCTGAAAAAGCCATCCAGCTCAGTAGCTTTCTCTGGGATAACTGTGA-	177
Qy	41	-GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVa	60
Db	178	TGAAGGGAAGACCTCGCGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATCGT	237
Qy	60	lProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLe	80
Db	238	TCCTGGAAATGTGACCTCAGTGTCTGGGCGAGCACAGTGTCTCCCTGAGTTCTCTCT	297
Qy	80	uLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysTh	100
Db	298	GAAGGTGGATTAGTTTGGAGAAGGAGGTGGCTCTGGATCAAGATCCCATGCAC	357
Qy	100	rAspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuLePr	120
Db	358	AGACTACATTGGCAGCTGTACCTTTGAAACACTTCTGTGATGTCTTGACATGTTAATTC	417
Qy	120	oThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPh	140
Db	418	TACTGGGAGCCCTGCCAGAGCCCTGCGTACCTATGGCTTCTTGGCCTGCTCCCTT	477
Qy	140	eLysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuP	160
Db	478	CMAAGAGGAACCTACTCTACCTGCCAAGAGCGAATTCTGTGTGATGTCTTGACATGTTAATTC	536
Qy	160	roSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerGlyLysA	180
Db	537	CCAGTTGGCTCACCCAGGAACTACCGATAGAGAGCGCTCTGAGCAGCAGTGGGAGC	596
Qy	180	rgLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle	193
Db	597	GTCTGGGCTGCATCAAGATCGTCTCTCTAAAGGGCATA	637

US-10-030-937-9 (1-193) x US-10-843-641A-1447 (1-2436)			
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Db	59	ATGCAGTCCCTGATGCAGGCTCCCTCTGATCGCCCTGGCTTGTCTTCGGGACCCCT	118
Qy	21	AlaGlnAlaHisLeuLysProSerGlnLeuSerSerPheSerTrpAspAsnCysPhe	40
Db	119	GCGCAAGCCACCTGAAAAAGCCATCCAGCTCAGTAGCTTTCTCTGGGATAACTGTGA-	177
Qy	41	-GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVa	60
Db	178	TGAAGGGAAGACCTCGCGTGATCAGAAGCCTGACTCTGGAGCCTGACCCCATCGT	237
Qy	60	lProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLe	80
Db	238	TCCTGGAAATGTGACCTCAGTGTCTGGGCGAGCACAGTGTCTCCCTGAGTTCTCTCT	297
Qy	80	uLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysTh	100
Db	298	GAAGGTGGATTAGTTTGGAGAAGGAGGTGGCTCTGGATCAAGATCCCATGCAC	357
Qy	100	rAspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuLePr	120
Db	358	AGACTACATTGGCAGCTGTACCTTTGAAACACTTCTGTGATGTCTTGACATGTTAATTC	417
Qy	120	oThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPh	140
Db	418	TACTGGGAGCCCTGCCAGAGCCCTGCGTACCTATGGCTTCTTGGCCTGCTCCCTT	477
Qy	140	eLysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuP	160
Db	478	CMAAGAGGAACCTACTCTACCTGCCAAGAGCGAATTCTGTGTGATGTCTTGACATGTTAATTC	536
Qy	160	roSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerGlyLysA	180
Db	537	CCAGTTGGCTCACCCAGGAACTACCGATAGAGAGCGCTCTGAGCAGCAGTGGGAGC	596
Qy	180	rgLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle	193
Db	597	GTCTGGGCTGCATCAAGATCGTCTCTCTAAAGGGCATA	637

RESULT 6			
US-10-843-641A-1447			
; Sequence 1447, Application US/10843641A			
; Publication No. US20050064454A1			
; GENERAL INFORMATION:			
; APPLICANT: Avalon Pharmaceuticals, Inc.			
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using			
; TITLE OF INVENTION: Signature Gene Sets			
; FILE REFERENCE: 689290-189			
; CURRENT APPLICATION NUMBER: US/10/843,641A			
; CURRENT FILING DATE: 2004-05-12			
; PRIOR APPLICATION NUMBER: US/09/873,367			
; PRIOR FILING DATE: 2001-06-05			
; PRIOR APPLICATION NUMBER: US/09/954,531			
; PRIOR FILING DATE: 2001-09-18			
; PRIOR APPLICATION NUMBER: US/09/954,456			
; PRIOR FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US/09/962,436			
; PRIOR FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US/09/962,832			
; PRIOR FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US/09/964,824			
; PRIOR FILING DATE: 2001-09-27			
; PRIOR APPLICATION NUMBER: US/09/967,768			
; PRIOR FILING DATE: 2001-09-28			

RESULT 7			
US-10-170-385-390			
; Sequence 390, Application US/10170385			
; Publication No. US20030203372A1			
; GENERAL INFORMATION:			
; APPLICANT: Ward, Neil Raymond			
; APPLICANT: Mundy, Christopher Robert			
; APPLICANT: Kan, On			

```

; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268200100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 2478
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-190

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Alignment Scores:	
Pred. No.:	3.85e-102
Score:	112.00
Percent Similarity:	97.95%
Best Local Similarity:	97.95%
Query Match:	58.03%
DB:	17
	Gaps: 0
	Indels: 4
	Mismatches: 2
	Conservative: 0
	Matches: 191
	Length: 2478

US-10-030-937-9 (1-193) x US-10-170-385-390 (1-2478)

Qy		1	MetGlnSerLeuWetGlnIaPProLeuLeuLeuLeuAlaThrPro	20
Dd		96	ATGCAGTCCCTCATGCAGCTCCCCCTCCTGATCGCCCTGGGCTTGCTTC	155
Qy		21	AlaGlnAlaHisLeuLysValysProSerGlnLeuSerSerPheSerTrpAspAenCysPhe	40
Dd		156	GCGCAAGCCACCTGAANAAGCATCCCAAGCTCAGTAGCTTTCTCTGGGAAACTGTGA-	214
Qy		41	-GlUyGLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVa	60
Dd		215	TGAAGGGAAGGACCCTGCCGTGATCAGAAGCCTGCATCTGGAGCGTGACCCCATCGTCGT	274
Qy		60	LProGlyAenValThrLeuSerValValGlySerThrServaIProLeuSerSerProIe	80
Dd		275	TCCTGAAATGTGACCCCTCAGTGTCTGGGAGAGCACAGAGTGTCCCCTCGATTCTCTCT	334
Qy		80	uLysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCynth	100
Dd		335	GAAGGTGGATTTAGTTTTGGAGAAGAGGTGGCTTGCCCTCTGGATCAAGATCCCATGGAC	394
Qy		100	rAspTryIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeullePr	120
Dd		395	AGACTACATTGGCAGCTGTACTTGTGAACA CTCTGTGATGTGCTGCATGTTAATTCC	454
Qy		120	oThrGlyGluProCysProGluProLeuArgThrTyTrGlyLeuProCysHisCysProPh	140
Dd		455	TACTGGGAGCCCTGCCAGAGCCCTCGTACCCTATGGGCTCTCTTGCCACTGTCCCTT	514
Qy		140	eLysGluGlyThrTyTrSerLeuProLysSerGluPheala - ValProAspLeuGluLeup	160
Dd		515	CAAAAGAAGNA CCTACTCACTGCCCAAGAGGAATTCTGTGTGCTTGACTCGAGCTGC	573
Qy		160	roSerTrpLeuThrThrGlyAenTyArqIleGluSerValLeuSerSerSerGlyLysa	180
Dd		574	CCAGTGGCTCACCACCGGAAC TACC CATAGAGAGCGTCTCTGAGCAGCAGTGGGAGC	633
Qy		180	rgLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle	193
Dd		634	GTCTGGGCTGCATCAAGATCGTGCTCTCTTAAGGGGCATA	674

RESULT 8

```

US-10-723-860-5187
; Sequence 5187, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5187
; LENGTH: 3988
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2864)..(2894)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3472)..(3486)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-5187

```

Alignment Scores:		
Pred. No.:	5.92e-102	3988
Score:	112.00	152
Percent Similarity:	98.70%	Conservative: 0
Best Local Similarity:	98.70%	Mismatches: 1
Query Match:	98.03%	Indels: 0
DB:	20	Gaps: 2

US-10-030-937-9 (1-193) x US-10-723-860-5187 (1-3988)

Qy	41	GluGlyLysAspProAlaValIleArgSerLeuThrLeuGluProAspProIleValVal	60
Db	216	GAAGGGAAGGACCCCTCGCGTGATCAGAAGCGCTGACTCTGGAGGCTGACCCCATCGTCGTT	275
Qy	61	ProGlyAsnValThrLeuSerValValGlySerThrSerValProLeuSerSerProLeu	80
Db	276	CCTGGAAATGTGACCCTCAGTGTCTGGGAGCACCAGTGTCCCCCTAGTTCCTCTCTG	335
Qy	81	LysValAspLeuValLeuGluLysGluValAlaGlyLeuTrpIleLysIleProCysThr	100
Db	336	AAGSTGGATTTAGTTTTCGAGAAGGAGTGGCTGGCCCTCTGGATCAAGATCCCATGCACA	395
Qy	101	AspTyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIlePro	120
Db	396	GACTACATTGGCAGCTGTACCTTTGAAACACTTCTGTGATGTGTGCATGTTAAATTCCT	455
Qy	121	ThrGlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPhe	140
Db	456	ACTGGGGAGCCCTGCCCAGAGCCCCCTGGTACCTATGGGCTTCTTGGCCACTGTCCCTTC	515
Qy	141	LysGluGlyThrTyrSerLeuProLysSerGluPheAla-ValProAspLeuGluLeuPr	160
Db	516	AAAGAAGGAACCTACTCATCTCCCAAGAGCGAAATTCGT-TGTGCTTGACCTGGAGCTGCC	574
Qy	160	oSerTrpLeuThrThrGlyAsnTyrArgIleGluSerValLeuSerSerSerGlyLysAr	180
Db	575	CAGTTGGCTCACCAACCGGAACTACCCGCATAGAGCGTCTCTGAGCAGCAGTGGGAGCG	634
Qy	180	gluGlyCysIleLysIleAlaAlaSerLeuLysGlyIle	193
Db	635	TCTGGGCTGCATCAAGATCGCTGCCTCTCTAAAGGGCATA	674

RESULT 9
US-09-864-761-1518/c
; Sequence 1518, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1518
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: MAP TO AC011342.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
US-09-864-761-1518
Alignment Scores: 1.69e-51 Length: 475
Pred. No.: 61.00 Matches: 61
Score:

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 31.61% Indels: 0
DB: 9 Gaps: 0
US-10-030-937-9 (1-193) x US-09-864-761-1518 (1-475)
QY 82 ValAspLeuValLeuGluLysGluValAlaGlyLeuTrrpIleLysIleProCysThrAsp 101
Db 465 GTGGATTAGTTTGGAGAGGAGGTGGCTGGCTCAAGATCCATGCCACAGAC 406
QY 102 TyrIleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIleProThr 121
Db 405 TACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGCTTGACATGTTAATTCCTACT 346
QY 122 GlyGluProCysProGluProLeuArgThrTyrGlyLeuProCysHisCysProPheLys 141
Db 345 GGGGAGCCCTGCCAGAGCCCTGGCTACCTATGGCTTCCTTGCACATGTCCTTCAAA 286
QY 142 Glu 142
Db 285 GAA 283
RESULT 10
US-09-864-761-18277/c
; Sequence 18277, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29

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/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 18277
/ LENGTH: 145
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC011342.1
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 11
/ OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
/ OTHER INFORMATION: EST_HUMAN HIT: BE182886.1, EVALUE 2.00e-76
/ OTHER INFORMATION: SWISSPROT HIT: P17900, EVALUE 7.00e-25
/ OTHER INFORMATION: NT HIT: X16087.1, EVALUE 2.00e-76
US-09-864-761-18277
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Alignment Scores:
Pred. No.: 6,86e-39 Length: 145
Score: 48.00 Matches: 48
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 24.87% Indels: 0
DB: 9 Gaps: 0
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US-10-030-937-9 (1-193) x US-09-864-761-18277 (1-145)

```
QY 82 ValAspLeuValLeuGluLysGluValAlaGlyLeuTrieLysIleProCysThrAsp 101
DB 145 GTGGATTAGTTTGGAGAGAGGTTGGCTTGGATCAGATCCATGCCAGAC 86
QY 102 TyrlleGlySerCysThrPheGluHisPheCysAspValLeuAspMetLeuIleProThr 121
DB 85 TACATTGGCAGCTGTACCTTTGAACACTTCTGTGATGTGCTTGACATGTTAATTCCTACT 26
QY 122 GlyCysProCysProGluProLeu 129
DB 25 GGGGAGCCCTGCCAGAGCCCTG 2
```

```
RESULT 11
US-09-969-034-4215
/ Sequence 4215, Application US/09969034
/ Publication No. US20040110668A1
/ GENERAL INFORMATION:
/ APPLICANT: Burgess, Christopher C.
/ APPLICANT: Astle, Jon H.
/ APPLICANT: Carroll, Eddie III
/ APPLICANT: Catino, Theodore J.
/ APPLICANT: Dwivedi, Poornima
/ APPLICANT: Molino, Gary A.
/ APPLICANT: Thiagalangam, Arunthathi
/ APPLICANT: Lewis, Marcia E.
/ TITLE OF INVENTION: Nucleic Acid Sequences Differentially
/ FILE REFERENCE: 1657/1032
/ CURRENT APPLICATION NUMBER: US/09/969,034
/ CURRENT FILING DATE: 2001-10-02
/ PRIOR APPLICATION NUMBER: 60/237,271
/ PRIOR FILING DATE: 2000-02-10
/ NUMBER OF SEQ ID NOS: 4494
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4215
/ LENGTH: 448
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
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/ LOCATION: 241, 277, 288, 295, 299, 300, 304, 310, 316, 343, 346, 356,
/ LOCATION: 364, 370, 396, 406, 410, 415, 424, 437
/ OTHER INFORMATION: n = A,T,C or G
US-09-969-034-4215
```

```
Alignment Scores:
Pred. No.: 2,11e-30 Length: 448
Score: 40.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.73% Indels: 0
DB: 11 Gaps: 0
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US-10-030-937-9 (1-193) x US-09-969-034-4215 (1-448)

```
QY 154 ValProAspLeuGluLeuProSerTrpLeuThrThrGlyAsnTyzArgIleGluSerVal 173
DB 70 GTGCCTGACCTGGAGCTGCCAGTTGGCTCACCCGGGAAGTACCGCATAGAGCGTC 129
QY 174 LeuSerSerSerGlyLysArgLeuGlyCysIleLysIleAlaAlaSerLeuLysGlyIle 193
DB 130 CTGAGCAGCAGTGGGAAGCGTCTGGGCTGCATCAAGATCGTGCCTCTCTNAAGGCGATA 189
```

RESULT 12

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US-10-225-810-26/C
/ Sequence 26, Application US/10225810
/ Publication No. US20030157512A1
/ GENERAL INFORMATION:
/ APPLICANT: Birmingham, Jr., John R.
/ TITLE OF INVENTION: Transdorins and Methods of Using Tramdorin
/ FILE REFERENCE: McLaugh-07165
/ CURRENT APPLICATION NUMBER: US/10/225,810
/ CURRENT FILING DATE: 2002-08-21
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 26
/ LENGTH: 250000
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (33774)...(33774)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (42953)...(43052)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (45557)...(45656)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (48203)...(48302)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (49551)...(49650)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (51561)...(51660)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (52722)...(52821)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (53864)...(53963)
/ OTHER INFORMATION: n is a, c, g, or t
/ FEATURE:
/ NAME/KEY: misc_feature
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; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207800
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-207800

```

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Alignment Scores:
Pred. No.: 3.35e-08 Length: 546
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.33% Indels: 0
DB: 13 Gaps: 0

```

US-10-030-937-9 (1-193) x US-10-027-632-207800 (1-546)

```

Qy 41 GluGlyValAspProAlaValIleArgSerLeuThrLeuGluProAspProfile 58
Db 297 GAAGGGAAGGACCCCTGGGTGATCAGAAAGCCTGACTCTGGAGCCTGACCCCATC 350

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Search completed: July 28, 2005, 02:06:19
Job time : 1211.74 secs

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